

GenCore version 5.1.6  
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tein search, using sw model  
March 18, 2004, 13:24:49 ; Search time 21 Seconds  
(without alignments)  
1067.268 Million cell updates/sec

US-09-909-005-1  
1170  
1 MLKPSVTSAPADNATLVV.....LL1000000000CTOONHMS 233

BLOSUM62  
Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

hits satisfying chosen parameters: 283366

length: 0

length: 200000000

Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

PIR 78:★

1: pir1:\*

2: pir2: \*

```
3: pir3:*
4: pir4:*
```

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

## SUMMARIES

#	Query	Match	Length	DB	ID	Description
56.6	317	2	T27179			hypothetical prote
20.0	1131	2	T15617			hypothetical prote
18.7	852	2	T10811			channel associated
18.6	870	2	G01974			channel associated
17.8	960	1	A39651			discs-large tumor
16.8	720	2	A45436			synapse-associated
16.8	724	2	JH0800			postsynaptic densi
16.8	767	2	T09599			postsynaptic densi
16.4	904	2	I38757			homolog of Drosoph
16.4	911	2	I56552			synapse-associated
16.4	926	2	I38755			homolog of Drosoph
16.4	2055	2	T30259			multiple PBZ domai
15.9	2054	2	T46612			multi PBZ domain p
15.1	1012	2	T23160			hypothetical prote
15.0	431	2	T16191			hypothetical prote
14.8	2450	2	S71625			protein-tyrosine-p
14.7	2466	2	I67629			protein-tyrosine-p
14.4	2294	2	I67630			protein-tyrosine-p
14.3	117	2	I81209			tyrosine phosphata
14.3	126	2	I81210			tyrosine phosphata
14.1	1171	2	T42372			probable guanlylate
14.1	1256	2	JE0209			brain-specific ang
14.1	2490	1	A54971			protein-tyrosine-p
13.8	1337	2	T13948			atypical protein k
13.6	578	2	T21345			hypothetical prote
13.2	390	2	T26806			hypothetical prote
13.2	423	2	T21570			hypothetical prote
13.2	440	2	T21568			hypothetical prote
12.9	538	2	I59291			betal-syntrophin -

30	151	12.9	628	2	T09458
31	151	12.9	728	2	T09457
32	151	12.9	1112	2	T32733
33	151	12.9	1277	2	T14152
34	150.5	12.9	87	2	S60345
35	147.5	12.6	488	2	T51379
36	147.5	12.6	505	2	A53214
37	146.5	12.5	503	2	I84771
38	145.5	12.4	505	2	S62894
39	145.5	12.4	1893	2	A56158
40	144.5	12.4	450	2	G01158
41	144.5	12.4	1281	2	T00346
42	142.5	12.2	358	2	I46532
43	140.5	12.0	1095	2	T43275
44	138.5	11.8	2172	2	T00145
45	137.5	11.8	624	2	T19630

## ALIGNMENTS

RESULT 1  
T27179  
Hypothetical protein Y5G11A.10 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-C  
C:Accession: T27179  
R:Wallis, J.  
submitted to the EMBL Data Library, December 1998  
A:Reference number: D20322  
A:Accession: T27179  
A:Status: Preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-317 <WIL>  
A:Cross-references: EMBL:AL034488; NID:el1359895; PIN:CAA22459.1; CE  
A:Experimental source: Clone Y5G11A  
C:Genetics:  
A:Gene: CRSP:Y5G11A.10  
A:Introns: 55/3; 108/3; 175/3; 228/2; 253/3

Query Match 56.6%; Score 662; DB 2; Length 317;  
Best Local Similarity 68.4%; Pred. No. 2.5e-42;  
Matches 130; Conservative 30; Mismatches 30; Indels 0;

Qy	25	LDRVRAAIELLEKLBQSEGVVPHKLOSLKKVLQSEFCTAJREVYQVMEHTITV
Db	117	LERDYQRIELMEHVOKTGEVNNAKLASLQVLQSEFFGAVREVYETVYESIDF
Qy	85	RARATAKATAVAAFAAASEGHSGHSPRVVELPKTDEGLGFWMGCKEONSPYISRII
Db	177	KAAATAKATAVAAFAAAGAHAPRIVEJPKTDQGLGFWMGCKEONSPYISRII
Qy	145	RHGGLKRGDQLLSWNGVSVGEHEHKEKAVELLKAAKDSVKLVVRYTPPKVLEEMEA
Db	237	RHGGLKRGDQLLIANGVNVYAECAEKEKAVDLLKASVGSVKLVIRYWPVKLJDEMEF
Qy	205	TARREQOQQL 214
Db	297	IRSTOOSPTL 306

```

RESULT 2
T15617
hypothetical protein C25F6.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-9
C.Accession: T15617
R.Bentley, D.
submitted to the EMBL Data Library, October 1995
A.Description: the sequence of C. elegans cosmid C25F6.
A.Reference number: 218377
A.Accession: T15617
A.Status: preliminary; translated from GB/EMBL/DDBJ

```

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C:Genetics:
A:Gene: ChapSyn-110
C:Superfamily: discs-large tumor suppressor; GLGF domain homology; g9;
F:198-276/Domain: GLGF domain homology <GLG2>
F:543-601/Domain: SH3 homology <SH3>
F:681-858/Domain: guanylate kinase homology <GK1>

Query Match 18.6%; Score 217.5; DB 2; Length 870;
Best Local Similarity 29.3%; Pred. No. 1.7e-08;
Matches 55; Conservative 31; Mismatches 59; Indels 43;

QY 43 GEPVPHKIQSLKKVQSEFCTAIRVEYQVMHTITVNGCPFEFRATAKATAVAAI
Db 385 GLLPDSEMTS-----HSQSHSTATRQPSMTLQRAVSLLEG-----
QY 103 HSHPRVVELPKTDEGLGFGNVMGKEQNSPIYISRIIPGVAERHGLKRGDQILA
Db 418 --EPRKVLVHKSGTGLGFNIYVG--EDGEGIFVSFFLAGGPADLSGELQKGDQILA
QY 163 VEGEHEHKAVELLKAADSVKLVVYRTPKVLSEMAEAFPEKLK-----
Db 475 LRGASHEQAALAKGAGQTVIIAQYQPEDYARPEAKTHDLRQMNHSMSSGSI
QY 210 QQQQLLIQ 217
Db 535 QKRSLYVR 542

RESULT 5
A39631
discs-large tumor suppressor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-S-
C:Accession: A39631
R:Woods, D.F.; Bryant, P.J.
Cell 66, 451-464, 1991
A:Title: The discs-large tumor suppressor gene of Drosophila encodes
A:Reference number: A39651; MUID:91330294; PMID:1651169
A:Accession: A39651
A:Molecule type: mRNA
A:Residues: 1-960 <WOO>
A:Cross-references: GB:W73529; NID:g157243; PIDN:AAA28468.1; PID:g15
C:Comment: Loss of this protein causes large imaginal disks by allow
ction to control cellular proliferation.
C:Genetics:
A:Gene: FlyBase:dlgl1
A:Cross-references: FlyBase:FBgn001624
C:Superfamily: discs-large tumor suppressor; GLGF domain homology; g9;
C:Keywords: signal transduction
F:45-123/Domain: GLGF domain homology <GLG1>
F:159-241/Domain: GLGF domain homology <GLG2>
F:491-563/Domain: GLGF domain homology <GLG3>
F:607-665/Domain: SH3 homology <SH3>
F:771-948/Domain: guanylate kinase homology <GK1>

Query Match 17.8%; Score 208.5; DB 1; Length 960;
Best Local Similarity 39.3%; Pred. No. 9e-08;
Matches 46; Conservative 21; Mismatches 49; Indels 1;

QY 88 ATAKATVAAPAAEGSHSPRVVLPKTDGLGFNVMGKEQNSPIYISRIIPGG
Db 466 AVPPGTPRAVSTEDITREPTTITIKGPGQGLGFNIYVG--EDGQGIYVSPILAGG
QY 148 GLKRGDQLLSVNGSVGEHHEKAVELLKAADSVKLVVYRTPKVLSEMAEAFPE
Db 525 ELKRGDQLLSVNNVNLTHATHEAAQALTKSGGVVLLAQYRPEEYNRFEARIQ

RESULT 6
A5436
synapse-associated protein SAP90 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-J

```

[illegible]

sity protein PSD-95 - rat  
s: brain specific PSD-95 protein; discs-large tumor suppressor protein h  
s: norvegicus (Norway rat)  
1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999  
800; S26407  
t, C.A.; Kennedy, M.B.  
2, 1992  
brain postsynaptic density fraction contains a homolog of the drosophila  
er: JH0800; MUID:93040233; PMID:1419001  
800  
mRNA  
4 <CHO>  
es: GB:M96853; NID:g206454; PIDN:ABA41971.1; PID:g206455  
orbs; brain  
discs-large tumor suppressor; GLGF domain homology; guanylate kinase homo  
: GLGF domain homology <GLG1>  
: GLGF domain homology <GLG2>  
: SH3 homology <SH3>  
: quanylate kinase homology <GK1>

16.8%; Score 196.5; DB.2; Length 724;  
 ilarity 41.4%; Pred.No.5.1e-07;  
 Conservative 19; Mismatches 38; Indels 1; Gaps 1;  
 VVELPKTDEGLGNVWGKBNQSPYIYSRIIPGVAERHGLKRGDQLLSVNGVSWG 165  
 RIVIRHGSTGLGFGNIYVG--EDGEGIFSTIFLAGGPADISGLKQDQLSVNGVDLRN 369  
 HEKAVELIKAAKDSVKLVVRVTPKVLSEMEARFEKL 204  
 HEQAAITAKNAGOTVITIAQYKPEYSRFEAKIDLR 408

usity protein 95 - human  
sapiens (man)  
1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jan-2000  
1599  
; Hoover, K.H.; You, Z.; Bryant, P.J.  
; ENBL Data Library, July 1998

A:Reference number: Z16761  
A:Accession: T09599  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: i-767 >STA>  
A:Cross-references: EMBL:U83192; NID:g3318652; PTD:g3318653  
A:Experimental source: mammary  
C:Genetics:  
A:Gene: PSD95  
C:Superfamily: discs-large tumor suppressor; GUGF domain homology; g  
F:208-286/Domain: GLGF domain homology <GLG>  
F:478-536/Domain: SH3 homology <SH3>  
F:578-755/Domain: guanylate kinase homology <GKI>

Query Match 16.8%; Score 196.5; DB 2; Length 767;  
Best Local Similarity 41.4%; Pred. No. 5.4e-07;  
Matches 41; Conservative 19; Mismatches 38; Indels 1;

QY 106 PRVPELPKDEGLGFNVMGKEQNSPITYISRIIPGVVAERHGGLRGDQLLSVN  
||| : : ||| : | : ||| : | : ||| : | : ||| :  
Db 354 PRRIIVHRGTSLGFNVGG-EDGEGIFSFILAGGPADLSGELRKGDIILSN  
||| : : ||| : | : ||| : | : ||| : | : ||| :  
QY 166 EHHEKAVELLKAAKDSVKLVTRYTPKVLEMEAREKL 204  
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db 413 ASHQEQATALKNAGQTWTIIAQYPEYSRFKATHDL 451  
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

```

RESULT 9
138757
homolog of Drosophila discs large protein, isoform 1 - human
C:Species: Homo sapiens (man)
C>Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-J
C:Accession: I38757
R:Rue, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994
A:Title: Cloning and characterization of hdlg: the human homologue c
A:Reference number: I38756; MUID:95024052; PMID:7937897
A:Accession: I38757
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-904 <RES>
A:Cross-references: EMBL:U13897; NID:G558437; PIDN:AAA50599.1; PID:G
C:Genetics:
A:Gene: GDB:DLG1
A:Cross-references: GDB:393278; OMIM:601014
A:Map position: 3q29-3q29
C:Superfamily: discs-large tumor suppressor; GLGF domain homology; G
C:Keywords: alternative splicing; duplication
F:229-307/Domain: GLGF domain homology <GLGF>
F:324-402/Domain: GLGF domain homology <GLGF>
F:588-646/Domain: SH3 homology <SH3>
F:715-892/Domain: guanylate kinase homology <GKI>

```

Query Match	16.4%;	Score 192;	DB 2;	Length 904;
Best Local Similarity	35.2%;	Pred. No. 1.4e-06;		
Matches	44;	Conservative 23;	Mismatches 44;	Indels 14;
Qy	106	PRVLEPKTDGELGFMVGGKEQNSPIYISRIIPGGVAERHGGKLRGDDQLLSV		
Db	464	PRKVIHRRGSGTGLGFNVGG-EDGEGIFISFIAGFAGPDLGELURKGRIRISV		
Qy	166	EHHEKAVELLAAKDSVKLVWRYTPPKVLEMEARFEKLR-----TV		
Db	523	ASHEQAAALNAGQAVTIVAQYRPEEVSFPEAKIHDLREQMNSSISSGSGSI		
Qy	213	QLLIQ 217		
Db	583	SLYVR 587		

RESULT 10  
I56552.  
synapse-associated protein 97 - rat

QY	213 QLLIQ 217  :: DB 583 SLVVR 587
RESULT 12	
T30259	multiple PDZ domain protein - mouse
C:Species:	Mus musculus (house mouse)
C>Date:	22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-J
C:Accession:	T30259
R:Simpson,	B.H.; Suffolk, R.; Jackson, I.J.
Genomics 59,	102-104, 1999
A>Title:	Identification, sequence, and mapping of mouse multiple PDZ
A:Reference number:	#20797; MUID:99326529; PMID:10395806
A:Accession:	T30259
A>Status:	preliminary; translated from GB/EMBL/DBJ
A:Molecule type:	mRNA
A:Residues:	1-2055 <STM>
A:Cross-references:	EMBL:AJ131869; NID:g4150877; PIDN:CAA10523.1; PI
A:Experimental source:	strain C57/BL6 X CBA F1; whole brain
C:Genetics:	
A:Gene:	mpdz
A:Map position:	4
Query Match	16.4%; Score 191.5; DB 2; Length 2055;
Best Local Similarity	29.0%; Pred. No. 4.2e-06;
Matches 56; Conservative 31; Mismatches 81; Indels 25;	
QY	1 MLKPVSPTSAPTADMAT---LTVVPQLTLDRVARAIELLEKLQESGEVPVHKL
DB	1879 MMHPGVAAQTOKLRVGDRVITCGTSDGTHTOAVNLKMNASGSIEVOVVAG
QY	57 LOSEFCTAIRREVYQMHEFTIIVNGCEPFRARATAXATAVAAPASEGHSHPRIVE
DB	1939 TG-----HQELANFLAF----TGLTSSIFPDLDGPSQSKEITT
QY	117 GLGFNVWGG---KEONSPIYSRIIPGVAEHBGLKGDDLSLVNGSVSVEGEH
DB	1981 GUSFNIGVYGSGPHGDLPITYKTFAKGAADGRLEKRGDQITAVNGQSLGEGVT
QY	174 LTKAAKDSVKLVV 186
DB	2041 ILKRTKGVIILMV 2053
RESULT 13	
T46612	multi PDZ domain protein 1 - rat
C:Species:	Rattus norvegicus (Norway rat)
C>Date:	18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-J
C:Accession:	T46612
R:Ullmer,	C.; Schmuck, K.; Figge, A.; Lubbert, H.
FEBB Lett.	424, 63-68, 1998
A>Title:	Cloning and characterization of MuPP1, a novel PDZ domain p
A:Reference number:	Z23104; MUID:98196865; PMID:9537516
A:Accession:	T46612
A>Status:	preliminary; translated from GB/EMBL/DBJ
A:Molecule type:	mRNA
A:Residues:	1-2054 <ULL>
A:Cross-references:	EMBL:AJ001320; NID:g2959978; PIDN:CAA04681.1; PI
A:Experimental source:	brain
C:Genetics:	
A:Gene:	MUPP1
Query Match	15.9%; Score 186.5; DB 2; Length 2054;
Best Local Similarity	28.5%; Pred. No. 9.9e-06;
Matches 55; Conservative 31; Mismatches 82; Indels 25;	
QY	1 MLKPVSPTSAPTADMAT---LTVVPQLTLDRVARAIELLEKLQESGEVPVHKL
DB	1878 MMHPGVAAQTOKLRVGDRVITCGTSDGTHTOAVNLKMNASGSIEVOVVAG

us-09-909-005-1.rpr

Search completed: March 18, 2004, 13:28:52  
Job time : 21 secs

.1. GENES  
 es: EMBL:U49829; NID:gl203924; PFD:gl203931; PIDN:AAA93388.1; CESP:F27D9  
 D9.8  
 52/3; 74/1; 96/1; 128/2; 149/3; 199/2; 255/3; 297/3; 319/3; 350/3; 390/3  
 alarity  
 15.0%; Score 176; DB 2; Length 431;  
 Pred. NO. 9.3e-06.

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protein search, using sw model

March 18, 2004, 13:21:24 ; Search time 18 Seconds  
(without alignments)

674.019 Million cell updates/sec

US-09-909-005-1

1170

1 MKPSVTSFPTADMTLVV.....LLIQQQQQQQQQQQQQNHS 233

BLOSUM62

Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues

hits satisfying chosen parameters: 141681

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SwissProt\_42:\*

is the number of results predicted by chance to have a  
ater than or equal to the score of the result being printed,  
rived by analysis of the total score distribution.

#### SUMMARIES

Query	Match	Length	DB	ID	Description
18.7	852	1	DLG2_RAT	Q63622	rattus norv
18.6	870	1	DLG2_HUMAN	Q15700	homo sapien
17.8	960	1	DLG1_DROME	P31007	drosophila
17.4	817	1	DLG3_HUMAN	Q92796	homo sapien
17.4	849	1	DLG3_MOUSE	P70175	mus musculus
17.4	849	1	DLG3_RAT	Q62936	rattus norv
16.8	724	1	DLG4_MOUSE	Q62108	mus musculus
16.8	724	1	DLG4_RAT	P31016	rattus norv
16.8	767	1	DLG4_HUMAN	P78352	homo sapien
16.4	904	1	DLG1_HUMAN	Q12959	homo sapien
16.4	911	1	DLG1_RAT	Q62696	rattus norv
14.4	2485	1	PTND_HUMAN	Q12923	homo sapien
14.3	1356	1	PAD3_HUMAN	Q8tew0	homo sapien
13.8	1333	1	PAD3_MOUSE	Q99nh2	mus musculus
13.8	1337	1	PAD3_RAT	Q92340	rattus norv
13.7	540	1	SNB2_HUMAN	Q13425	homo sapien
13.5	520	1	SNB2_MOUSE	Q61235	mus musculus
13.5	537	1	SNB1_MOUSE	Q99188	mus musculus
13.5	637	1	MPP4_HUMAN	Q96jb8	homo sapien
13.5	206	1	SJ2B_RAT	Q9wj74	rattus norv
13.4	539	1	STG2_HUMAN	Q9ny99	homo sapien
13.2	631	1	IL16_HUMAN	Q14005	homo sapien
13.2	631	1	IL16_PANTR	Q62666	pan troglod
13.0	145	1	SJ2B_HUMAN	P57105	homo sapien
13.0	910	1	US1C_MOUSE	Q9es64	mus musculus
12.9	538	1	SNB1_HUMAN	Q13884	homo sapien
12.9	728	1	LNK1_MOUSE	O70263	mus musculus
12.9	1275	1	AIP1_MOUSE	Q9wvq1	mus musculus
12.9	1275	1	AIP1_RAT	O88382	rattus norv
12.9	1455	1	AIP1_HUMAN	Q8cul8	homo sapien
12.6	539	1	STG2_MOUSE	Q225e0	mus musculus
12.6	728	1	LNK1_HUMAN	Q8tbb1	homo sapien
12.6	505	1	SNAI_RABIT	Q28626	oryctolagus

34	146.5	12.5	503	1	SNAI_MOUSE	Q61234	m
35	145.5	12.4	505	1	SNAI_HUMAN	Q13424	h
36	145.5	12.4	552	1	US1C_HUMAN	Q9y6n9	h
37	144.5	12.4	1809	1	DLG5_HUMAN	Q8cdm6	h
38	143.5	12.3	742	1	NEB1_HUMAN	Q9ulj8	h
39	140.5	12.0	687	1	LNK2_MOUSE	Q91xl2	m
40	140.5	12.0	1095	1	NEB1_RAT	O35867	r
41	137.5	11.8	1026	1	PTPI_CAEL	P28191	c
42	137.5	11.8	1815	1	SHK3_RAT	O9jlu4	r
43	137	11.7	1205	1	PAL3_HUMAN	Q8cew8	h
44	136.5	11.7	690	1	LNK2_HUMAN	Q8n448	h
45	134	11.5	517	1	STG1_HUMAN	Q9n8n8	h

#### ALIGNMENTS

RESULT 1  
DLG2\_RAT  
ID DLG2\_RAT STANDARD; PRT; 852 AA.  
AC Q63622; P70548; Q62939;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Channel associated protein of synapse-110 (Chapsyn-110) (Synap  
density protein PSD-93) (Discs, large homolog 2).  
GN DLG2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
OX NCBI TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96310881; PubMed=8755482;  
RA Kim E., Cho K.O., Rothschild A., Sheng M.;  
RT "Heteromultimerization and NMDA receptor-clustering activity o  
Chapsyn-110, a member of the PSD-95 family of proteins.";  
RL Neuron 17:1103-113(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96193770; PubMed=8625413;  
RA Brennan J.E., Chao D.S., Gee S.H., McGee A.W., Craven S.E.,  
RA Santillano D.R., Wu Z., Huang F., Xia H., Peters M.F.,  
RA Froehner S.C., Bredt D.S.;  
RT "Interaction of nitric oxide synthase with the postsynaptic de  
protein PSD-95 and alpha1-syntrophin mediated by PDZ domains."  
RL Cell 84:757-767(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX Irie M., Hata Y., Takai Y.;  
RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECE  
SUBUNITS AS WELL AS POTASSIUM CHANNELS.  
CC -!- SIMILARITY: Belongs to the MAGUK family.  
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.  
CC This SWISS-PROT entry is copyright. It is produced through a c  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U49049; AAB53243.1; -;  
CC EMBL; U50717; AAC52643.1; -;  
CC EMBL; U53368; AAB48562.1; -;  
CC PIR; T10811; T10811.  
CC HSPF; Q12959; IPDR.  
CC InterPro; IPR008144; Guanylate kin.  
CC InterPro; IPR008145; Guanylt/Ca.

```

RN RP SEQUENCE FROM N.A.
RX MEDLINE=96310881; PubMed=8755482;
RA Kim E., Cho K.-O., Rothschild A., Sheng M.;
RT "Heteromultimerization and NMDA receptor-clustering activity of
RT Chapsyn-110, a member of the PSD-95 family of proteins.";
RL Neuron 17:103-113(1996).
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR
CC SUBUNITS AS WELL AS POTASSIUM CHANNELS.
CC -!- SIMILARITY: Belongs to the MAGUK family.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC -----
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CC the European Bioinformatics Institute. There are no restricti
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CC modified and this statement is not removed. Usage by and for
CC entities requires a license agreement (See http://www.isb-sib.c
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U32376; AB04949.1; -.
DR PIR; G01974; G01974.
DR HSSP; Q12959; 1PDR.
DR Genew; HGNC:2901; DLG2.
DR MIM; 603583; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004385; F:guanylate kinase activity; TAS.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR008145; Guanylt/Ca.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 3.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00072; GuK; 1.
DR SMART; SM00228; PDZ; 3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS00552; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS0106; PDZ; 3.
DR PROSITE; PS00002; SH3; 1.
KW SH3 domain; Repeat.
FT DOMAIN 98 184 PDZ 1.
FT DOMAIN 193 279 PDZ 2.
FT DOMAIN 421 501 PDZ 3.
FT DOMAIN 536 606 SH3.
FT DOMAIN 680 870 GUANYLATE KINASE.
SQ SEQUENCE 870 AA; 97500 MW; 89C83BA0619F6F59 CRC64;

Query Match 18.6%; Score 217.5; DB 1; Length 870;
Best Local Similarity 29.3%; Pred.No.2.9e-08;
Matches 55; Conservative 31; Mismatches 59; Indels 43;

QY 43 GEVPHKQLSLKVLQSEFCTAIREVYQYMHETITVNGCPFRARATAKATVAI
Db 385 GLLPSEMTS-----HSQHSTATQPSMTLQRAVSLEG-----
QY 103 HSHPRVVELPKTDEGLGFNWMGKEQNSPIYISRIIPGVVAERHGLKRGDQLI
Db 418 --EPRKVVLRHKGSTGLGFNIVGG-EDGEGIFVSVILAGGPADLSGELQRGDQII
QY 163 VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLMEAEARFEKLK-----
Db 475 LRASGHEQAALKGAGQVTIIAQYQPEDYARFEAKIHDLREOMHNSMSSGE
QY 210 QQOQLLIQ 217
Db 535 QKRSUYVR 542

```

STANDARD; PRT; 960 AA.

(Rel. 26, Created)  
 (Rel. 26, Last sequence update)  
 (Rel. 42, Last annotation update)  
 -1 tumor suppressor protein.  
 DLG1.  
 melanogaster (Fruit fly).  
 Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;  
 Drosophilidae; Drosophila.  
 7227;

DM N.A., AND FUNCTION.

FO;

30294; PubMed=1651169;

Bryant P.J.;

large tumor suppressor gene of Drosophila encodes a  
 kinase homolog localized at septate junctions.;

-464(1991).

N: Plays a critical role at septate junctions in cellular  
 control during larval development. The presence of a  
 kinase domain suggests involvement in cellular adhesion  
 as signal transduction to control cellular proliferation.  
 for maintenance of cell polarity.

JULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE  
 SMIC FACE OF THE MEMBRANE IN THE CELLULAR ELASTODERM AND  
 ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM  
 EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT  
 LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF  
 TIAL CELLS.

TIVE PRODUCTS:

Alternative splicing; Named isoforms-1;  
 at=A number of isoforms are produced;

=P31007-1; Sequence=Displayed;

SPECIFICITY: In embryos, expression is seen in epithelial  
 and some nervous tissue. In larvae, expression is seen as a  
 round salivary glands and imaginal disks, also in  
 rictulus and parts of the brain. Expressed in adult  
 ctive tissues.

MENTAL STAGE: Expressed both maternally and zygotically  
 out development.

ITY: Belongs to the MAGUK family.

ITY: Contains 3 PDZ/DHR domains.

ITY: Contains 1 SH3 domain.

ITY: Contains 1 guanylate kinase-like domain.

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 n-profit institutions as long as its content is in no way  
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 quires a license agreement (See <http://www.isb-sib.ch/announce/>  
 email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

9; AAA28468.1; --

; A39651.

6; 18FE.

gn0001624; dlgl.

179; C:apical cortex; IDA.

327; C:apicolateral plasma membrane; IDA.

948; C:septate junction; NAS.

175; P:basal protein localization; IMP.

391; P:dorsal closure; NAS.

197; P:establishment and/or maintenance of epithel. . .; NAS.

334; P:establishment and/or maintenance of polarit. . .; IGI.

336; P:establishment and/or maintenance of polarit. . .; NAS.

399; P:neurogenesis; IMP.

273; P:regulation of synapse; IMP.

PR008144; Guanylate\_kin.

DR InterPro; IPR008145; Guanylt/Ca.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00625; Guanylate\_kin; 1.  
 DR Pfam; PF00595; PDZ; 3.  
 DR Pfam; PF00018; SH3; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00072; GuKc; 1.  
 DR SMART; SM00228; PDZ; 3.  
 DR SMART; SM00336; SH3; 1.  
 DR PROSITE; PS00856; GUANYLATE\_KINASE\_1; 1.  
 DR PROSITE; PS00052; GUANYLATE\_KINASE\_2; 1.  
 DR PROSITE; PS0106; PDZ; 3.  
 DR PROSITE; PS00002; SH3; 1.  
 KW Transducer; SH3 domain; Alternative splicing; Repeat.  
 FT DOMAIN 40 126 PDZ 1.  
 FT DOMAIN 154 244 PDZ 2.  
 FT DOMAIN 486 566 PDZ 3.  
 FT DOMAIN 600 670 SH3.  
 FT DOMAIN 768 960 GUANYLATE\_KINASE.  
 SQ SEQUENCE 960 AA; 102468 MW; BF87A4262F1B6AD5 CRC64;

Query Match 17.8%; Score 208.5; DB 1; Length 960;  
 Best Local Similarity 39.3%; Pred. No. 1.4e-07;  
 Matches 46; Conservative 21; Mismatches 49; Indels 1;

QY 88 ATAKATVAFAAEGSHPRVVELPKTDEGLGNVNGGKQNSPIYISRIIPGG  
 DB 466 AVPTPTFANSTEDITREPRITITKQPGQLGNIVGG-EDGQGIYVSFILAGG  
 QY 148 GLKRGDQLLSVNGSVSGEHEKAVELLKAADSVKLVRVYTPKVLSEMEARFE  
 DB 525 ELKRGDQLLSVNNVNLTHATHEAAQALKTSGGVVTLLAQYRPEYNRFEARIQ

## RESULT 4

DLG3 HUMAN STANDARD; PRT; 817 AA.  
 ID DLG3 HUMAN Q9ULI8;  
 AC Q92736; Q9ULI8;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE Presynaptic protein SAP102 (Synapse-associated protein 102)  
 DE 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE (Neuroendocrine-DLG) (NE-DLG) (Disks, large homolog 3).  
 GN DLG3 OR KIAA1232.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Petal brain;  
 RX MEDLINE=97332623; PubMed=9188857;  
 RA Makino K., Kawahara H., Masuko N., Nishiyama Y., Morisaki T.,  
 RA Sasaki J., Nakano M., Kuwano A., Nakata M., Ushio Y., Saya H.;  
 RT "Cloning and characterization of NE-dlg: a novel human homolog  
 RT Drosophila discs large (dlg) tumor suppressor protein interacts  
 RT the APC protein.";  
 RL Oncogene 14:2425-2433 (1997).  
 RN [2]  
 RP SEQUENCE OF 330-817 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039619; PubMed=10574462;  
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes  
 RT The complete sequences of 100 new cDNA clones from brain which  
 RT for large proteins in vitro.";  
 RL DNA Res. 6:337-345(1999).  
 CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA R  
 CC SUBUNIT NR2B (BY SIMILARITY).  
 CC -!- SIMILARITY: Belongs to the MAGUK family.  
 CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.



```

[1]
RN      SEQUENCE FROM N.A.
RP      STRAIN=C57BL/6; TISSUE=Brain;
RC      Kohmura N., Makino S., Yagi T.;
RR      Submitted (AUG-1996) to the EMBL/GenBank/DBST databases.
CC      -1- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA R
CC      SUBUNIT NR2B.
CC      -1- SIMILARITY: Belongs to the MAGUK family.
CC      -1- SIMILARITY: Contains 3 PDZ/DHR domains.
CC      -1- SIMILARITY: Contains 1 SH3 domain.
CC      -1- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC      -----
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! SIMILARITY: Contains 1 guanylate kinase-like domain.

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utheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
10116;

OM N.A. (ISOFORM LONG).

74358; PubMed=8780649;  
i., Kistner U., Kindler S., Chung W.J., Kuhlendahl S.,  
i., Lau L.-F., Veh R.W., Haganir R.L., Gundelfinger E.D.,  
i. novel postsynaptic protein that interacts with NMDA  
complexes in vivo.;;  
55-265(1996).

OM N.A. (ISOFORM SHORT).

ta Y., Takai Y.;  
SEP-1996) to the EMBL/GenBank/DBJ databases.  
N: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR  
' NK2B.

ITVE PRODUCTS:

alternative splicing; Named isoforms=2;

ng;  
i=062936-1; Sequence=Displayed;

ort;  
i=Q62936-2; Sequence=VSP 003151;

ITY: Belongs to the MAGUK family.

ITY: Contains 3 PDZ/DHR domains.

ITY: Contains 1 SH3 domain.

ITY: Contains 1 guanylate kinase-like domain.

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email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

7; AAA93031.1; -

7; AAB48561.1; -

9; 1PDR.

PRO08144; Guanylate\_kin.

PRO08145; Guanylt/Ca.

PRO01478; PDZ.

PRO01452; SH3.

25; Guanylate\_kin; 1.

95; PDZ; 3.

18; SH3; 1.

100066; SH3; 1.

1072; GuK; 1.

1228; PDZ; 3.

326; SH3; 1.

100856; GUANYLATE\_KINASE\_1; 1.

150052; GUANYLATE\_KINASE\_2; 1.

150106; PDZ; 3.

150002; SH3; 1.

Repeat; Alternative splicing.

149 235 PDZ 1.

244 330 PDZ 2.

404 484 PDZ 3.

519 589 SH3.

659 849 GUANYLATE\_KINASE.

627 640 Missing (in isoform Short).

849 AA; 93539 MW; 34DA9C46C7BB96DB CRC64;

ilarity 17.4%; Score 203.5; DB 1; Length 849;

Conservative 18; Mismatches 37; Indels 1; Gaps 1;

RVELPKTDEGLGVMSGEQNSPIYISRIIPGGVAERHGGKRGDQLLSVNGSVSEG 165

XKILHKGSTGLGVNIVGG-EDGEGIFV8FILLAGGPADLSGELRRGDRILLSVNGVNLRN 460

QY 166 EHHEKAVELLKAAKSDSVKLVRVYTPKVLERNMEARFEKLR 204  
Db 461 ATHEQAAAAAKRAGOSVTIVAQYRPEEYSRFSKIHDLR 499

RESULT 7

DLG4 MOUSE

ID DLG4 MOUSE STANDARD; PRT; 724 AA.

AC Q62108;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Presynaptic density protein 95 (PSD-95) (Presynaptic protein 95

GN DLG4 OR DLGH4 OR PSD95.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2; TISSUE=Brain;

RA Kohmura N., Yagi T.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Interacts with the cytoplasmic tail of NMDA recept

CC subunits. May be involved in synaptogenesis.

CC -!- SUBUNIT: Interacts with DLGAP1/GKAP and with KCND2 (By

CC or SHANK3 (By similarity). Interacts through its third PDZ

CC with NLGN1, and probably with NLGN2 and NLGN3. Interacts th

CC its first PDZ domain with GRK2, KCNA4 and CRIPT. Interacts th

CC through its second PDZ domain with NOS1 and CAPON (By simi

CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic

CC junctions primarily on the presynaptic side. Also found in

CC postsynaptic density of neuronal cells (By similarity).

CC -!- SIMILARITY: Belongs to the MAGUK family.

CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.

CC -!- SIMILARITY: Contains 1 SH3 domain.

CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.

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CC the European Bioinformatics Institute. There are no restrict

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CC -----

DR EMBL; D50621; BAA09297.1; -

DR HSP; P31016; 1BE9.

DR MGD; MG1:1277959; DlgH4.

DR InterPro; IPR008144; Guanylate\_kin.

DR InterPro; IPR008145; Guanylt/Ca.

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00625; Guanylate\_kin; 1.

DR Pfam; PF00595; PDZ; 3.

DR Pfam; PF00018; SH3; 1.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00072; GuK; 1.

DR SMART; SM00228; PDZ; 3.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS00856; GUANYLATE\_KINASE\_1; 1.

DR PROSITE; PS00852; GUANYLATE\_KINASE\_2; 1.

DR PROSITE; PSS0106; PDZ; 3.

DR PROSITE; PSS0002; SH3; 1.

KW SH3 domain; Repeat.

FT DOMAIN 65 151 PDZ 1.

FT DOMAIN 160 246 PDZ 2.

FT DOMAIN 313 393 PDZ 3.

FT DOMAIN 428 498 SH3.

FT DOMAIN 534 724 GUANYLATE\_KINASE.

SEQUENCE 724 AA; 80472 MW; 7EFFC99E1FF90BA CRC64;

16.8%; Score 196.5; DB 1; Length 724;  
 ilarity 41.4%; Pred. No. 7.5e-07;  
 Conservative 19; Mismatches 38; Indels 1; Gaps 1;  
 VVELPKTDEGLGNVNGKQNSPIYISRIIPGVVAERHGLKKGQQLLSVNGSVVEG 165  
 RIVIRHGSTGLGNVIGG-EDGEGIFISFILAGPADLSGELRKQDQLLSVNGVDLRN 369  
 HEKAVELKKAKOSVXLVRYTPKVLSEMEAREFKLR 204  
 HEQAAIAIKNAGQVTITIAQYKPEYSRFEAKIHDLR 408  
 STANDARD; PRT; 724 AA.  
 631;  
 (Rel. 26, Created)  
 (Rel. 26, Last sequence update)  
 (Rel. 43, Last annotation update)  
 density protein 95 (PSD-95) (Presynaptic protein SAP90)  
 sociated protein 90 (Discs, large homolog 4).  
 95.  
 egicus (Rat).  
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 utheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 10116;  
 OM N.A.  
 que-Dawley; TISSUE=Brain;  
 86749; PubMed=7680343;  
 Wenzel B.M., Veh R.W., Cases-Langhoff C., Garner A.M.,  
 U., Voss B., Gundelfinger E.D., Garner C.C.;  
 at presynaptic protein related to the product of the  
 tumor suppressor gene dlG-A.";  
 em. 268:4580-4583 (1993).  
 ' 566-625 FROM N.A.  
 ar Kyoto; TISSUE=Vascular smooth muscle;  
 Werry I., Schwartz S.M.;  
 NOV-1996) to the EMBL/GenBank/DBJ databases.  
 ; WITH DLGAP1 AND SHANK PROTEINS.  
 58653; PubMed=10527873;  
 M., Winter C., Smalla K.-H., Kreutz M.R., Bockmann J.,  
 r C., Garner C.C., Gundelfinger E.D.;  
 ch synapse-associated proteins ProSAP1 and ProSAP2 interact  
 ic proteins of the SAPAP/GKAP family.";  
 ophys. Res. Commun. 264:247-252 (1999).  
 [ WITH KCND2.  
 37905; PubMed=11923279;  
 well E.W., Jugloff D.G.M., Jones O.T., Schlichter L.C.;  
 ice targeting and clustering interactions between  
 usly expressed PSD-95 and the Shal voltage-gated potassium  
 4.2.";  
 tem. 277:20423-20430 (2002).  
 'ALOGGRAPHY (1.82 ANGSTROMS) OF 302-402.  
 :70509; PubMed=8674113;  
 Lee A., Lewis J., Kim E., Sheng M., Mackinnon R.;  
 ructures of a complexed and peptide-free membrane protein-  
 ain: molecular basis of peptide recognition by PDZ.";  
 7-1076 (1996).

[7]  
 RN STRUCTURE BY NMR OF 155-246, AND INTERACTION WITH NOS1 AND CAPO  
 RP MEDLINE=20090929; PubMed=10623522;  
 RA Tochio H., Hung F., Li M., Bret D.S., Zhang M.;  
 RT "Solution structure and backbone dynamics of the second PDZ dom  
 RL post-synaptic density-95.";  
 RL J. Mol. Biol. 295:225-237 (2000).  
 [8]  
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 430-724.  
 RX MEDLINE=21638676; PubMed=11779504;  
 RA McGee A.W., Dakoji S.R., Olsen O., Bret D.S., Lim W.A., Prehod  
 RT "Structure of the SH3-guanylate kinase module from PSD-95 sugge  
 RL mechanism for regulated assembly of MAGUK scaffolding proteins.  
 RL Mol. Cell 8:1291-1301 (2001).  
 [9]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 430-724.  
 RX MEDLINE=21638678; PubMed=11779506;  
 RA Tavares G.A., Panepucci E.H., Bruner A.T.;  
 RT "Structural characterization of the intramolecular interaction  
 RL between the SH3 and guanylate kinase domains of PSD-95.";  
 RL Mol. Cell 8:1313-1325 (2001).  
 CC -!- FUNCTION: Interacts with the cytoplasmic tail of NMDA recep  
 CC subunits. May be involved in synaptogenesis.  
 CC -!- SUBUNIT: Interacts with DLGAP1/GKAP. Is part of a complex w  
 CC DLGAP1/GKAP, SHANK1, SHANK2 or SHANK3. Interacts through its  
 CC PDZ domain with NLGN1, and probably with NLGN2 and NLGN3. I  
 CC through its first PDZ domain with GRIK2, KCNA4 and CRIPT (B  
 CC similarity). Interacts through its second PDZ domain with N  
 CC CAPON. Interacts with KCND2.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic  
 CC junctions primarily on the presynaptic side. Also found in  
 CC post-synaptic density of neuronal cells.  
 CC -!- TISSUE SPECIFICITY: PRESYNAPTIC DENSITY FRACTION OF BRAIN.  
 CC -!- SIMILARITY: Belongs to the MAGUK family.  
 CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
 CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.  
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 DR EMBL; M96853; AAA41971.1; -;  
 DR EMBL; X66474; CAA47103.1; -;  
 DR EMBL; U77090; AAB38270.1; -;  
 DR PIR; JH0800; JH0800.  
 DR PDB; 1BE9; 21-OCT-98.  
 DR PDB; 1BFE; 21-OCT-98.  
 DR PDB; 1JXM; 16-JAN-02.  
 DR PDB; 1KJW; 01-MAY-02.  
 DR PDB; 1QLC; 06-FEB-00.  
 DR InterPro; IPR008144; Guanylate\_kin.  
 DR InterPro; IPR008145; Guanylt/Ca.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00625; Guanylate\_kin; 1.  
 DR Pfam; PF00595; PDZ; 3.  
 DR Pfam; PF00018; SH3; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00072; GuK; 1.  
 DR SMART; SM00228; PDZ; 3.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS00856; GUANYLATE\_KINASE\_1; 1.  
 DR PROSITE; PS00552; GUANYLATE\_KINASE\_2; 1.  
 DR PROSITE; PS0106; PDZ; 3.  
 DR PROSITE; PS00002; SH3; 1.  
 DR SH3 domain; Repeat; 3D-structure.  
 FT DOMAIN 65 151 PDZ 1.  
 FT DOMAIN 160 246 PDZ 2.



15:31:26 2004

us-09-909-005-1.rsp

```
16.8%; Score 196.5; DB 1; Length 767;
ilarity 41.4%; Pred. No. 8e-07;
Conservative 19; Mismatches 38; Indels 1; Gaps 1;
VELPKTDEGLGNMGKQNSPIYSRIIPGGVAERHGGKRGDQLLSVNGSVSE 165
: : ||||| : : : : : : : : : : : : : : : : : : : : : :
RVIHVGSTGLGNFVGG-EDGEGIFISFILAGGPADLSGELRKGDQLLSVNGVDLRN 412
HKAVELLKAAKOSVKLVVRYTPKVLMEAREFEKLR 204
|| : || : || : || : || : || : || : || : || : || : || : ||
HQAALAKNAGQTIIIAQYKPEYSRFEAKIHDR 451

STANDARD; PRT; 904 AA.
958;
(Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
protein SAP97 (Synapse-associated protein 97) (Discs,
og 1) (hdlg).
s (Human).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
utheria; Primates; Catarrhini; Hominidae; Homo.
9606;
OM N.A.
24052; PubMed=7937897;
ariatia S.M., Branton D., Chishti A.H.;
a characterization of hdlg: the human homologue of the
discs large tumor suppressor binds to protein 4.1.";
Acad. Sci. U.S.A. 91:9818-9822(1994).
ALLOGRAPHY (2.8 ANGSTROMS) OF 460-555.
38231; PubMed=8757139;
M., Chishti A.H., Sutcliffe M.J., Raza S., Byron O., Poy F.,
ructure of a PDZ domain.";
549-652(1996).
N: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR
S. ASSOCIATES WITH PROTEIN 4.1..
: Binds to KIF13B.
IIVE PRODUCTS:
lternative splicing; Named isoforms=2;
-Q12959-1; Sequence=Displayed;
-Q12959-2; Sequence=VSP_003150;
ITY: Belongs to the MAGUK family.
ITY: Contains 3 PDZ/DHR domains.
ITY: Contains 1 SH3 domain.
ITY: Contains 1 guanylate kinase-like domain.
-----
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email to license@isb-sib.ch).
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7; AAA50599.1; .
6; AAA50598.1; .
; I38756.
; I38757.
23-JUL-97.
;2900; DLGI.
; .
737; Cytoplasm; TAS.
911; C:intercellular junction; TAS.
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0; AAA79976.1; -.
      9; IPDR.
PR008144; Guanylate_kin.
PR008145; Guanylt/Ca.
PR004172; L27.
PR001478; PDZ.
PR001452; SH3.
25; Guanylate_kin; 1.
95; PDZ; 3.
18; SH3; 1.
00066; SH3; 1.
072; GuKc; 1.
589; L27; 1.
228; PDZ; 3.
326; SH3; 1.
00856; GUANYLATE_KINASE_1; 1.
50052; GUANYLATE_KINASE_2; 1.
50106; PDZ; 3.
50002; SH3; 1.
Repeat.
224 310 PDZ 1.
318 404 PDZ 2.
465 545 PDZ 3.
580 650 SH3..
721 911 GUANYLATE_KINASE.
527 530 POLY-ALA.
911 AA; 100570 MW; 18CEBD3IDDCAF8B CRC64;
16.4%; Score 192; DB 1; Length 911;
Similarity 35.2%; Pred.No. 2.1e-06;
Conservative 23; Mismatches 44; Indels 14; Gaps 15
VVELPKTDEGLGNWVGKEQNSPIYISRIIPGGVAERHCGIKRGDQLLSNVGSVEG 165
```

R.L., Feingold E.A., Grouse L.H., Derge J.G., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E., M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W., K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Telton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., W., Touchman J.W., Green E.D., Dickson M.C., C.C., Grimwood J., Schmutz J., Myers R.M., Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schein J.E., Jones S.J.M., Marra M.A.; and initial analysis of more than 15,000 full-length human DNA sequences." *Acad. Sci. U.S.A.* 99:16899-16903 (2002).

WITH TRIP6.  
29089; PubMed=10400701;  
Clark K., Fortin Y., Shen S.-H., Barville D.;  
Yin-related protein, interacts with the second PDZ domain  
solic protein tyrosine phosphatase hPTP1E.";  
em. 274:20679-20687 (1999).

WITH NGR.  
12928; PubMed=10544233;  
chiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,  
Bredesen D.E., Sato T.A.;  
interaction of Fas-associated phosphatase-1 (FAP-1) with  
d their effect on NF-kappaB activation.";  
460:191-198 (1999).

Y NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE  
OF TNFRSF6.  
70882; PubMed=10704206;  
Gehring K., Ekiel I.;  
structure of the PDZ2 domain from human phosphatase hPTP1E  
eractions with C-terminal peptides from the Fas  
Y 39:2572-2580 (2000).

Y NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE  
LEUCIDE EXCHANGE FACTOR RA-GEF-2.  
90786; PubMed=12095257;  
Banville D., Gehring K., Ekiel I.;  
structure of the PDZ2 domain from cytosolic human  
hPTP1E complexed with a peptide reveals contribution of  
eak3 loop to PDZ domain-ligand interactions.";  
1. 320:813-820 (2002).

O-1419 AND MET-1522.  
23362; PubMed=12436199;  
Harada H., Nagai H., Fukino K., Teramoto A., Emi M.;  
ad juxtaposition of Fas-associated phosphatase-1 (FAP-1)  
H2-terminal kinase 3 (JNK3) genes: genomic structure and  
orphisms of the FAP-1 gene.";  
et. 47:614-619 (2002).

N: Regulates negatively Fas-induced apoptosis and NGR-  
IC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
e + phosphate.  
: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through  
and PDZ domain. Interacts with the C-terminal SVP motif of  
rough its third PDZ domain.  
UAR LOCATION: Cytoplasmic (By similarity).  
TIVE PRODUCTS:  
lternative splicing; Named isoforms=4;  
=Q12923-1; Sequence=Displayed;

R.L., Feingold E.A., Grouse L.H., Derge J.G., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E., M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W., K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Telton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., W., Touchman J.W., Green E.D., Dickson M.C., C.C., Grimwood J., Schmutz J., Myers R.M., Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schein J.E., Jones S.J.M., Marra M.A.; and initial analysis of more than 15,000 full-length human DNA sequences." *Acad. Sci. U.S.A.* 99:16899-16903 (2002).

WITH TRIP6.  
29089; PubMed=10400701;  
Clark K., Fortin Y., Shen S.-H., Barville D.;  
Yin-related protein, interacts with the second PDZ domain  
solic protein tyrosine phosphatase hPTP1E.";  
em. 274:20679-20687 (1999).

WITH NGR.  
12928; PubMed=10544233;  
chiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,  
Bredesen D.E., Sato T.A.;  
interaction of Fas-associated phosphatase-1 (FAP-1) with  
d their effect on NF-kappaB activation.";  
460:191-198 (1999).

Y NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE  
OF TNFRSF6.  
70882; PubMed=10704206;  
Gehring K., Ekiel I.;  
structure of the PDZ2 domain from human phosphatase hPTP1E  
eractions with C-terminal peptides from the Fas  
Y 39:2572-2580 (2000).

Y NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE  
LEUCIDE EXCHANGE FACTOR RA-GEF-2.  
90786; PubMed=12095257;  
Banville D., Gehring K., Ekiel I.;  
structure of the PDZ2 domain from cytosolic human  
hPTP1E complexed with a peptide reveals contribution of  
eak3 loop to PDZ domain-ligand interactions.";  
1. 320:813-820 (2002).

O-1419 AND MET-1522.  
23362; PubMed=12436199;  
Harada H., Nagai H., Fukino K., Teramoto A., Emi M.;  
ad juxtaposition of Fas-associated phosphatase-1 (FAP-1)  
H2-terminal kinase 3 (JNK3) genes: genomic structure and  
orphisms of the FAP-1 gene.";  
et. 47:614-619 (2002).

N: Regulates negatively Fas-induced apoptosis and NGR-  
IC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
e + phosphate.  
: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through  
and PDZ domain. Interacts with the C-terminal SVP motif of  
rough its third PDZ domain.  
UAR LOCATION: Cytoplasmic (By similarity).  
TIVE PRODUCTS:  
lternative splicing; Named isoforms=4;  
=Q12923-1; Sequence=Displayed;

Names=2;  
IsoId=Q12923-2; Sequence=VSP\_000496;  
Names=3;  
IsoId=Q12923-3; Sequence=VSP\_000497;  
Names=4;  
IsoId=Q12923-4; Sequence=VSP\_007921;  
Note=May be due to a competing donor splice site;  
TISSUE SPECIFICITY: Present in most tissues with the except  
the liver and skeletal muscle. Most abundant in lung, kidney  
fecal brain.  
-!- SIMILARITY: Contains 1 FERM domain.  
-!- SIMILARITY: Contains 5 PDZ/DHR domains.  
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase fan  
Non-receptor class subfamily.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; U12128; AAB60339.1; -  
EMBL; D21209; BAA04750.1; -  
EMBL; D21210; BAA04751.1; -  
EMBL; D21211; BAA04752.1; -  
EMBL; X80289; CAA55563.1; -  
EMBL; X79676; CAA56124.1; -  
EMBL; L34583; AAC41755.1; -  
EMBL; AF233323; AAF63474.1; -  
EMBL; BC039610; AAH39610.1; ALT\_TERM.  
PIR; A54971; A54971.  
PIR; 167629; 167629.  
PIR; 167630; 167630.  
PDB; 3PDZ; 17-MAR-00.  
PDB; 1D5G; 24-JUL-02.  
Genew; HGNC:9646; PTPN13.  
MIM; 600267; -  
GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.  
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
InterPro; IPR000299; Band 4.1.  
InterPro; IPR001478; PDZ.  
InterPro; IPR000387; TYR phosphatase.  
InterPro; IPR000242; TYR\_PP.  
Pfam; PF00373; Band 41; 1.  
Pfam; PF00595; PDZ; 5.  
Pfam; PF00102; Y\_phosphatase; 1.  
PRINTS; PR00935; BAND41.  
PRINTS; PR00700; PRTYPHPTASE.  
SMART; SM00295; B41; 1.  
SMART; SM00228; PDZ; 5.  
SMART; SM00194; PTPC; 1.  
PROSITE; PS00660; FERM\_1; FALSE\_NEG.  
PROSITE; PS00661; FERM\_2; FALSE\_NEG.  
PROSITE; PS00507; FERM\_3; 1.  
PROSITE; PS0106; PDZ; 5.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structu  
Alternative splicing; Coiled coil; Polymorphism.  
FT DOMAIN 56 59 POLY-LEU.  
FT DOMAIN 572 872 FERM.  
FT DOMAIN 237 2485 PROTEIN-TYROSINE PHOSPHATASE.  
FT DOMAIN 379 399 COILED COIL (POTENTIAL).  
FT DOMAIN 469 504 COILED COIL (POTENTIAL).

Query Match 14.4%; Score 169; DB 1; Length 2485;  
Best Local Similarity 28.4%; Pred. No. 0.0003;  
Matches 40; Conservative 26; Mismatches 43; Indels 32;  
QY 78 VNGCFEPRABATAKATVAFAASEGSHPR-----

**RX** MEDLINE=21143360; PubMed=11149944;  
RA Eichmüller S., Ueener D., Dummer R., Stein A., Thiel D.,  
RA Schädendorf D.;  
**RT** "Serological detection of cutaneous T-cell lymphoma-associated  
antigens";  
**RL** Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).  
**RN** [7]  
**RP** SEQUENCE OF 857-1356 FROM N.A.  
**RC** TISSUE=Lung;  
**RX** MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner K.D., Collins F.S., Wagner L., Shenmen C.M., Schuler  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise P.  
RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheet  
Brownstein M.J., Usdin T.B., Toshikiyuki S., Carninci P., Prange  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huly,  
RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
FAhey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sancil  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalski S., Smallus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Barra M.A.;  
"Generation and initial analysis of more than 15,000 full-length  
and mouse cDNA sequences.";  
**RL** Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
**RN** [8]  
**RP** INTERACTION WITH PAR6A.  
**RX** MEDLINE=20411249; PubMed=10954424;  
RA Johansson A.-S., Drieskens M., Aspenstroem P.;  
**RT** "The mammalian homologue of the Caenorhabditis elegans polarity  
protein PAR-6 is a binding partner for the Rho GTPases Cdc42 at  
Racl.";  
**RL** J. Cell Biol. 113:3267-3275(2000).  
**RN** [9]  
**RP** SUBUNIT OF A COMPLEX CONTAINING PAR6B AND PRKCI.  
**RC** TISSUE=Kidney;  
**RX** MEDLINE=21157398; PubMed=11257119;  
RA Suzuki A., Yamana T., Hirose T., Manabe N., Mizuno K., Shimii,  
Akimoto K., Izumi Y., Ohnishi T., Ono S.;  
**RT** "Atypical protein kinase C is involved in the evolutionarily cy  
par protein complex and plays a critical role in establishing  
epithelia-specific junctional structures.";  
**RL** J. Cell Biol. 152:1183-1196(2001).  
**CC** -!- FUNCTION: Adapter protein involved in asymmetrical cell div:  
and cell polarization processes. Seems to play a central r  
the formation of epithelial tight junctions. Association w  
PAR6B may prevent the interaction of PAR3 with FLNR/JAM1,  
thereby preventing tight junction assembly. The PAR6-PAR3:  
complex links GIP-bound Rho small GTPases to atypical prote  
kinase C proteins.  
**CC** -!- SUBUNIT: Interacts with PAR6A and PAR6B. Isoform 2, but i  
least isoform 3 interacts with PRKCZ. Interacts with PRCKI  
similarity). Part of a complex with PAR6A or PAR6B, PRCKI  
PRKCZ and CDC42 or RACL. Interacts with FLNR/JAM1 [By simi]  
**CC** -!- SUBCELLULAR LOCATION: Cytoplasmic; membrane associated. Par  
localized along the cell-cell contact region. Colocalizes w  
PAR6A and PRKI at epithelial tight junctions.  
**-!** ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=10;  
Name=1; Synonyms=A;  
IsoId=Q8TEW0-1; Sequence=Displayed;  
Name=2; Synonyms=B, La;  
IsoId=Q8TEW0-2; Sequence=VSP\_007464;  
Name=3; Synonyms=C;  
IsoId=Q8TEW0-3; Sequence=VSP\_007465;  
Name=4; Synonyms=D;  
IsoId=Q8TEW0-4; Sequence=VSP\_007469;



Qy	86	APATKATVAAFAASGSHPRV-----VELPKTDEGLGFNV-----MGKKE
Db	434	APASAPQNVFTTSSGVNTTKKRLNKLKKGTEGLGFSITSRDVTIG--
Qy	135	SRIPGGVAERHGLKRGDQLLSVNGVSVEGHHKAAVELLKAAK--DSVKLVW
Db	491	KNILPRGNAITODRLKAGRLIEVNGVDLVGKSEQEVSLRSTKTEGVTSLLV

RESULT 14

ID	PAD3 MOUSE	PAD3 MOUSE	STANDARD;	PRT;	1333 AA.
AC	Q99NEH2				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DE	Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (Ephrin interacting protein) (PHIP).				
DE	PARD3 OR PAR3				
OS	Mus musculus (Mouse)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M				
NCBI	TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 3).				
RC	STRAIN=NIH Swiss; TISSUE=Embryo;				
RC	MEDLINE=99121117; PubMed=9920925;				
RA	Lin D., Gish G.D., Songyang Z., Fawson T.;				
RT	"The carboxyl terminus of B class ephrins constitutes a PDZ dom				
RT	binding motif.";				
RL	J. Biol. Chem. 274:3726-3733(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). SUBCELLULAR LOCATION,				
RP	PHOSPHORYLATION BY PRKCZ, INTERACTION WITH PRKCI AND PARD6A, SU				
RP	OF A COMPLEX CONTAINING PARD6A AND CDC42, AND MUTAGENESIS OF				
RC	824-SER--SER-826.				
RC	STRAIN=NIH Swiss;				
RC	MEDLINE=20394297; PubMed=10934475;				
RA	Lin D., Edwards A.S., Fawcett J.P., Mbamalu G., Scott J.D., Paw				
RT	"A mammalian PAR-3-PAR-6 complex implicated in Cdc42/Rac1 and a				
RT	signalling and cell polarity.";				
RL	Nat. Cell Biol. 2:540-547(2000).				
RN	[3]				
RP	INTERACTION WITH PARD6B, AND SUBUNIT OF A COMPLEX CONTAINING PA				
RP	PRCI AND CDC42.				
RC	MEDLINE=20394296; PubMed=10934474;				
RA	Joberty G., Petersen C., Gao L., Macara I.G.;				
RT	"The cell-polarity protein Par6 links Par3 and atypical protein				
RT	C to Cdc42.";				
RL	Nat. Cell Biol. 2:531-539(2000).				
RN	[4]				
RP	INTERACTION WITH F1LR.				
RC	MEDLINE=21340266; PubMed=11447115;				
RA	Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,				
RA	Meyer zu Bruckwedde M.-K., Ohno S., Vestweber D.;				
RT	"The cell polarity protein ASIP/Par-3 directly associates with				
RT	junctional adhesion molecule (JAM).";				
RL	EMBO J. 20:3738-3748(2001).				
RN	[5]				
RP	INTERACTION WITH F1LR AND PARD6B.				
RC	MEDLINE=21828709; PubMed=11839275;				
RA	Gao L., Joberty G., Macara I.G.;				
RT	"Assembly of epithelial tight junctions is negatively regulated				
RT	Par6.";				
RL	Curr. Biol. 12:221-225(2002).				

CC -!- FUNCTION: Adapter protein involved in asymmetrical cell divi  
and cell polarization processes. Plays a role in the format  
epithelial tight junctions. Association with PARD6B may pre  
the interaction of PAR3 with F1LR/JAM1, thereby preventing  
junction assembly. The PARD6-PAR3 complex links GTP-bound  
small GTPases to atypical protein kinase C proteins.  
-!- SUBUNIT: Interacts with PARD6A, PARD6B, PRKCI and PRKCZ. Pa

519 LAGKSQEEVSLIRSTKMEGTVSLIVFQBEAFHPR---EMNAPSPQMOTPKKE

RESULT 15

PAD3_RAT	PAD3_RAT	STANDARD;	PRT;	1337 AA.
AC	Q92340;			
DC	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (Atypical PKC specific binding protein) (ASBP).			
DE	PARD3 OR PAR3.			
GN	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; R			
OC	NCBI_TaxId:10116;			
OC	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PKCI AND			
RP	TISSUE=Fibroblast;			
RC	MEDLINE=98437350; PubMed=9763423;			
RC	Izumi Y., Hirose T., Tamai Y., Hirai S.-I., Nagashima Y., Fujim			
RA	Tabuse Y., Kempthorne K.J., Ohno S.;			
RA	"An atypical PKC directly associates and colocalizes at the epi			
RT	tight junction with ASIP, a mammalian homologue of Caenorhabdit			
RT	elegans polarity protein PAR-3. "			
RL	J. Cell Biol. 143:95-106(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND			
RP	PHOSPHORYLATION OF SER-827.			
RP	MEDLINE=22040490; PubMed=12045219;			
RC	Hirose T., Izumi Y., Nagashima Y., Tamai-Nagai Y., Kurihara H.,			
RA	Sakai T., Suzuki Y., Yamanaka T., Suzuki A., Mizuno K., Ohno S.			
RA	"Involvement of ASIP/PAR-3 in the promotion of epithelial tight			
RT	junction formation. "			
RL	J. Cell Sci. 115:2485-2495(2002).			
RL	-i- FUNCTION: Adapter protein involved in asymmetrical cell divi			
CC	and cell polarization processes. Seems to play a central ro			
CC	the formation of epithelial tight junctions. Association wi			
CC	PARD6B may prevent the interaction of PARD3 with FHLR/JAM1,			
CC	thereby preventing tight junction assembly. The PARD6-PARD3			
CC	complex links GTP-bound Rho small GTPases to atypical prote			
CC	kinase C proteins.			
CC	-i- SUBUNIT: Interacts with PARD6A, PARD6B and FHLR/JAM1 via it			
CC	domain (By similarity). Interacts with PKCI. Interacts wit			
CC	(Probable). Part of a complex with PARD6A or PARD6B, PKCI			
CC	PKCZ and CDC42 or RAC1 (By similarity).			
CC	-i- SUBCELLULAR LOCATION: Cytoplasmic; membrane associated. Loc			
CC	along the cell-cell contact region. Colocalizes with PKCZ			
CC	apical edge of tight junctions.			
CC	-i- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named isoforms-2;			
CC	Name=1; Synonyms=180 kDa;			
CC	Isoid=092340-1; Sequence=Displayed;			
CC	Name=2; Synonyms=150 kDa;			
CC	Isoid=092340-2; Sequence=VSP_007475;			
CC	-i- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in			
CC	glandular stomach, prostate, ovary and uterus. Isoform 1 is			
CC	expressed in brain, with a high expression in the cortex,			
CC	hippocampus and in the striatum. Isoform 2 is predominantly			
CC	expressed in intestinal epithelial cells, kidney and prosta			
CC	-i- PTM: Phosphorylated by PKCZ (By similarity). The phosphory			
CC	form is concentrated at the most apical tip of cell-cell co			
CC	during the initial phase of tight junction formation.			
CC	-i- SIMILARITY: Belongs to the PAR3 family.			
CC	-i- SIMILARITY: Contains 3 PDZ/DHR domains.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a co			
CC	between the Swiss Institute of Bioinformatics and the EMBL co			
CC	the European Bioinformatics Institute. There are no restricti			
CC	use by non-profit institutions as long as its content is			
CC	modified and this statement is not removed. Usage by and for			

549; BAA34216.1; -.  
; T13948.

PR001478; PDZ.

228: PDZ: 3.

Cell division

271 359

461 546  
500 575

712 936  
004 1040

1050	1082
1140	1170

1199 1222

827 827

ilarity 31.0%

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100

1000

## SYSTEMS REPOSITORY

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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FRANKLIN D. ROOSEVELT

. March 19 200

2)

15:31:26 2004

us-09-909-005-1.1.rspt

GenCore version 5.1.1.6  
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tein search, using sw model

March 18, 2004, 13:22:34 ; Search time 45 Seconds  
(without alignments)  
1633.683 Million cell updates/sec

US-09-909-005-1

1170  
1 MEKPSVTSAPTADMATLVV.....LLIQQQQQQQQQQQQQHMS 233

BLOSUM62

Gapop 10.0 , Gapext 0.5

1017041 segs, 315518202 residues

hits satisfying chosen parameters: 1017041

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPRTEMBL\_25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	233	4	014910		014910 homo sapien
92.1	219	11	Q92250		Q92250 rattus norv
90.3	211	11	Q8JZS0		Q8JZS0 mus musculu
69.6	197	4	Q9NUP9		Q9NUP9 homo sapien
69.6	197	11	Q88952		Q88952 mus musculu
69.4	197	13	Q7ZVU3		Q7ZVU3 xenopus lae
69.1	207	11	Q88951		Q88951 mus musculu
69.1	207	11	Q92252		Q92252 rattus norv
69.0	207	4	Q9HAP6		Q9HAP6 homo sapien
64.8	182	11	Q92251		Q92251 rattus norv
64.4	195	5	Q9VBY7		Q9VBY7 drosophila
58.5	244	5	Q8IMT8		Q8IMT8 schistosoma
55.4	171	5	Q17458		Q17458 caenorhabdi
55.3	316	5	Q9U245		Q9U245 caenorhabdi
55.0	297	5	P90976		P90976 caenorhabdi
20.0	967	5	Q9B179		Q9B179 caenorhabdi

17	233.5	20.0	1064	5	Q18165
18	220	18.8	946	5	Q7YXH8
19	219	18.7	852	11	Q91XM9
20	208.5	17.8	960	5	Q9VYZ4
21	208.5	17.8	960	5	Q9VYZ5
22	203.5	17.4	950	11	Q80TH1
23	199.5	17.1	403	11	Q8BSV4
24	199.5	17.1	455	11	Q9ET11
25	199.5	17.1	455	11	Q920R1
26	199.5	17.1	455	11	Q920R1
27	198.5	17.0	463	11	Q8BH60
28	198.5	17.0	464	4	Q969U8
29	196.5	16.8	721	11	Q91WJ1
30	192	16.4	893	11	Q8CGN7
31	192	16.4	905	11	Q811D0
32	191.5	16.4	2055	11	Q9Z1K3
33	190.5	16.3	873	13	Q7ZUM2
34	188.5	16.1	164	11	Q8C0H8
35	187.5	16.0	526	11	Q08783
36	187.5	16.0	1124	11	Q80ZY8
37	187.5	16.0	2055	11	Q8VBY0
38	187.5	16.0	2055	11	Q8VBY5
39	187.5	16.0	2055	11	Q8VBY6
40	186.5	15.9	2054	11	Q55164
41	186	15.9	200	13	Q90X35
42	185	15.8	927	11	Q62402
43	178.5	15.3	519	11	Q80TZ1
44	178.5	15.3	526	11	Q8K4T6
45	178.5	15.3	532	11	Q7TQL6

#### ALIGNMENTS

#### RESULT 1

014910	PRELIMINARY;	PRT;	233 AA.
ID	014910		
AC	014910;		
DT	01-JAN-1998 (TRENBLrel. 05, Created)		
DT	01-MAY-1999 (TRENBLrel. 10, Last sequence update)		
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)		
DE	VELI 1 (YAX interaction protein 33) (Fragment).		
GN	MALS-1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RX	MEDLINE=98424246; PubMed=9753324;		
RA	Butz S., Okamoto M., Sudhof T.C.;		
RT	"A tripartite protein complex with the potential to couple syna		
RT	vesicle exocytosis to cell adhesion in brain.";		
RL	Cell 94:773-782(1998).		
RN	[2]		
RP	SEQUENCE OF 32-233 FROM N.A.		
RA	Rousset R., Fabre S., Desbois C., Bantignies F., Jalinet P.;		
RL	Oncogene 15:0-0(1997).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99274724; PubMed=10341223;		
RA	Jo K., Derin R., Li M., Bredt D.S.;		
RT	"Characterization of MALS/Velis-1, -2, and -3: a family of mamm		
RT	LIN-7 homologs enriched at brain synapses in association with t		
RT	postsynaptic density-95/AMPA receptor postsynaptic complex.";		
RL	J. Neurosci. 19:4189-4199(1999).		
CC	-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.		
DR	EMBL; AF087693; AAC78481.1;		
DR	EMBL; AF028826; AAB84251.1;		
DR	EMBL; AF173081; AAD48500.1;		
DR	HSP; Q12923; 3PDZ.		
DR	Genew; HGNC:17787; LIN7A.		

15; F:protein binding; IPI.  
61; P:exocytosis; TAS.  
61; P:protein complex assembly; TAS.  
R004172; L27.  
R001478; PDZ.  
8; L27; 1.  
5; PDZ; 1.  
69; L27; 1.  
28; PDZ; 1.  
0106; PDZ; 1.  
1  
33 AA; 25997 MW; D8D05EF16A93BE7B CRC64;  
100.0%; Score 1170; DB 4; Length 233;  
Larity 100.0%; Pred. No. 2.2e-86;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
PSVTSAPTADMATITVVQPLTLDRDVARAIELEKIQESGEVPPVHKQLSKVKVQSE 60  
PSVTSAPTADMATITVVQPLTLDRDVARAIELEKIQESGEVPPVHKQLSKVKVQSE 60  
AIREVYQVWHITIVNGCFEPPARATATVAFAASEGSHPRVWELPKTDEGLGF 120  
AIREVYQVWHITIVNGCFEPPARATATVAFAASEGSHPRVWELPKTDEGLGF 120  
GGKEQNSPIYISRIIPGVAERHGGIKRGDQLLVNGSVSGEGEHKAVELLKAARD 180  
GGKEQNSPIYISRIIPGVAERHGGIKRGDQLLVNGSVSGEGEHKAVELLKAARD 180  
LVRYTPKVLSEMAREKILTRRRQQQLLTQQQQQQQQQQQQQQQQNHS 233  
LVRYTPKVLSEMAREKILTRRRQQQLLTQQQQQQQQQQQQQQQQNHS 233  
PRELIMINARY; PRT; 219 AA.  
(TEMBLrel. 10, Created)  
(TEMBLrel. 10, Last sequence update)  
(TEMBLrel. 24, Last annotation update)  
gicus (Rat).  
Chetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
0116;  
M N.A.  
9097; PubMed=10362251;  
a Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka H.,  
and characterization of mammalian homologues of  
is elegans lin-7: localization at cell-cell junctions.";  
2811-2817(1999).  
TY: CONTAINS 1 PDZ/DHR DOMAIN.  
35; AAC78074.1; -.  
; 3PDZ.  
42; P:intracellular signaling cascade; IEA.  
R004172; L27.  
R001478; PDZ.  
8; L27; 1.  
5; PDZ; 1.  
69; L27; 1.  
28; PDZ; 1.  
0106; PDZ; 1.  
0106; PDZ; 1.  
119 AA; 24549 MW; 6EB6AAFC5C1EC74 CRC64;  
92.1%; Score 1077.5; DB 11; Length 219;  
Larity 98.6%; Pred. No. 5.7e-79;  
Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
LTVVQPLTLDRDVARAIELEKIQESGEVPPVHKQLSKVKVQSEFCAIREVYQVWH 73

Db	66	SPEVRANATAKATVAFAASEGHSHPRVWELPKTEG:GFNMGKEQNSPIY
Qy	141	GVAERHGLKRGDQLLSVNGSVSGEHEHKAVELLKAADKSVKLVRVY:PKVLE
Db	126	GIADRHGGLKRGDQLLSVNGSVSGEHEHKAVELLKAQGRKVLVRY:PKVLE
Qy	201	EKLRTARRQO 211
Db	186	EMVRSKRRQO 196
RESULT 5		
ID	088952	PRELIMINARY; PRT; 197 AA.
AC	088952;	
DT	01-NOV-1998 (TReMBLrel. 08, Created)	
DT	01-JAN-1999 (TReMBLrel. 09, Last sequence update)	
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)	
DE	VEL1 3 protein (Vertebrate homolog of C. elegans Lin-7 type 3) homolog C).	
GN	Lin7C OR VEL13 OR WAL5-3.	
OS	Mus musculus (Mouse), and	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; N	
OX	NCBI_TaxID=10090, 10116;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RP	SPECIES=Mouse; TISSUE=Heart;	
RC	MEDLINE=98424246; PubMed=9753324;	
RC	Butz S., Okamoto M., Sudhof T.C.;	
RT	"A tripartite protein complex with the potential to couple syna	
RT	vesicle exocytosis to cell adhesion in brain.";	
RT	Cell 94:773-782(1998).	
RL	[2]	
RP	SEQUENCE FROM N.A.	
RP	SPECIES=Rat;	
RC	Irie M., Hata Y., Deguchi M., Ide N., Hirao K., Yao I., Nishio	
RA	Takai Y.;	
RA	"Isolation and Characterization of Mammalian Homologues of	
RT	Cacophony in Drosophila: Localization at Cell-Cell Junction	
RT	Oncogene 0:0-0(1999).	
RL	[3]	
RP	SEQUENCE FROM N.A.	
RP	SPECIES=Mouse;	
RC	MEDLINE=99274724; PubMed=103414223;	
RC	Jo K., Derin R., Li M., Bredt D.S.;	
RA	"Characterization of WAL5/Vel1-1, -2, and -3: a family of mam	
RT	Lin-7 homologs enriched at brain synapses in association with t	
RT	postsynaptic density-95/NMDA receptor postsynaptic complex.";	
RT	J. Neurosci. 19:4189-4199(1999).	
RL	[4]	
RP	SEQUENCE FROM N.A.	
RP	SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Testis;	
RC	MEDLINE=21085660; PubMed=11217851;	
RC	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii	
RA	Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda	
RA	Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka	
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kaekawa T., Saito	
RA	Kadota K., Matsuda H.A., Aeburner M., Bataillon S., Casavant T.,	
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbu	
RA	Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., West	
RA	Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Baresi G.	
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.	
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.	
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.	
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts F	
RA	Nordone P., Ring B., Schoenbach C., Rodriguez I., Sakamoto N.,	
RA	Sasaki H., Sato K., Ringwald C., Seya T., Shibata Y., Storch	
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilm	
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohrsk	

Y.;  
annotation of a full-length mouse cDNA collection.;  
585-690(2001).

3M N.A.

se; STRAIN=C57BL/6J; TISSUE=Cecum;  
54683; PubMed=12466851;

Consortium,  
anome Exploration Research Group Phase I & II Team;  
f the mouse transcriptome based on functional annotation of  
length cDNAs.;  
563-573 (2002).

3M N.A.

se; TISSUE=Eye;

38257; PubMed=12477932;  
3.L., Feingold E.A., Grouse L.H., Derge J.G.,  
J., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
J., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
J., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
J.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
Joquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
alton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
W., Touchman J.W., Green E.D., Dickson M.C.,  
C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
Marra M.A.;  
and initial analysis of more than 15,000 full-length human  
cDNA sequences.";  
Acad. Sci. U.S.A. 99:16899-16903(2002).

3M N.A.

se; TISSUE=Eye;

38257; PubMed=12477932;  
3.L., Feingold E.A., Grouse L.H., Derge J.G.,  
J., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
J., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
J., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
J.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
Joquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
alton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
W., Touchman J.W., Green E.D., Dickson M.C.,  
C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
Marra M.A.;  
and initial analysis of more than 15,000 full-length human  
cDNA sequences.";  
Acad. Sci. U.S.A. 99:16899-16903(2002).

3M N.A.

se; TISSUE=Eye;

38257; PubMed=12477932;  
3.L., Feingold E.A., Grouse L.H., Derge J.G.,  
J., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
J., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
J., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
J.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
Joquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
alton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
W., Touchman J.W., Green E.D., Dickson M.C.,  
C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
Marra M.A.;  
and initial analysis of more than 15,000 full-length human  
cDNA sequences.";  
Acad. Sci. U.S.A. 99:16899-16903(2002).

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Marra M.A.;  
and initial analysis of more than 15,000 full-length human  
cDNA sequences.";  
Acad. Sci. U.S.A. 99:16899-16903(2002).

OY 201 EKLRTARRROQ 211  
Db 186 EKMRSKRROQ 196

RESULT 6

Q7ZYU3 PRELIMINARY; PRT; 197 AA.  
ID O7ZYU3;  
AC O7ZYU3;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to lin 7 homolog c (C. elegans).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.;  
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.  
RE EMBL; BC041249; AAH41249.1; -.  
RG GO:0007242; P:intracellular signaling cascade; IEA.  
DR InterPro; IPR004172; L27.  
DR InterPro; IPR001478; PDZ.  
DR Pfam; PF02828; L27; 1.  
DR Pfam; PF00595; PDZ; 1.  
DR SMART; SM00569; L27; 1.  
DR SMART; SM00228; PDZ; 1.  
DR PROSITE; PS01016; PDZ; 1.  
SQ SEQUENCE 197 AA; 21889 MW; F25BEF4A1219E87A CRC64;

Query Match 59.4%; Score 812; DB 13; Length 197;  
Best Local Similarity 79.8%; Pred. No. 1.2e-57;  
Matches 154; Conservative 25; Mismatches 14; Indels 0;

OY 19 VVQPLTDRDVARAELEKQESGVPVHKQSLKVLQSEFCTAIREVYQYM  
Db 4 VGEFVRLERDILRALEKQESGVPVHKQSLKVLQSEFCTAIREVYQYM  
OY 79 NCPEFRARATKATVAFAAASEGHSHPRVVELPKTDGLGFGNVMGKQESQFI  
Db 64 SSSPEVRANATKATVAFAAASEGHSHPRVVELPKTDGLGFGNVMGKQESQFI  
OY 139 PGVAERHGLKQESGVPVHKQSLKVLQSEFCTAIREVYQYM  
Db 124 PGIAERHGLKQESGVPVHKQSLKVLQSEFCTAIREVYQYM  
OY 199 RFEKLTARRROQ 211  
Db 184 RFEKLTARRROQ 196

RESULT 7

O88951 PRELIMINARY; PRT; 207 AA.  
ID O88951;  
AC O88951;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE VELI 2 (Vertebrate homolog of C. elegans Lin-7 type 2).  
GN LIN7B OR VELI2 OR MALS-2.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=98424246; PubMed=9753324;  
RA Butz S., Okamoto M., Sudhof T.C.;  
RT "A tripartite protein complex with the potential to couple synap

3; 3PDZ.  
242; P:intracellular signaling cascade; IEA.

14 MATLTIVVPIETIDDDVAPATPIETKIQECSCEVDVNHKI QSIKVKI QSEECTATPDE" matches 15//; Conservative 24; Mismatches 1//; Indels 2;

[illegible]



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AL--VEFLGLRVDVSRVALLERLQSGELPPOKLOALQVQLQSRFCSSAIRREVQY 58
ITVNGCFEPRARATKATVAFAASEGHSHPRVVELPKTDGLGFGFNVGKGQNSPIY 133
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
LDITGSABIRAHATKATVAFTAEGHAHPRVVELPKTDGLGFGFNVGKGQNSPIY 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RIIPGVAERHGLKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RVIPGVADRHGLKRGDQLLSVNGSVGEHHEKAVELLKAAQGSVKLVVRYTPRVL 178
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VEARFEKLTARBRQOQ 213
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VEARFEKRSARRQOQ 198
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

PRELIMINARY; PRT; 182 AA.

(TREMBLrel. 10, Created)
(TREMBLrel. 10, Last sequence update)
(TREMBLrel. 24, Last annotation update)

agizos; (Rat)
Metazoa; Craniata; Vertebrata; Euteleostomi;
Ichtheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
10116;

JM N.A.
39097; PubMed=10362251;
-a Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka H.,
and characterization of mammalian homologues of
his elegans lin-7: localization at cell-cell junctions. ";
:2811-2817(1999).
ITY: CONTAINS 1 PDZ/DHR DOMAIN.
134; AAC78073.1; --
3; 3PDZ.
242; P:intracellular signaling cascade; IEA.
PR004172; L27.
PR001478; PDZ.
28; L27; 1.
35; PDZ; 1.
369; L27; 1.
228; PDZ; 1.
30106; PDZ; 1.
182 AA; 19927 MW; D448E3BBCFSA51DB CRC64;

64.8%; Score 758; DB 11; Length 182;
ilarity 98.7%; Pred.No.2.5e-53;
Conservative 2; Mismatches 0; Indels 0; Gaps 0;

ELTVVQPLTLDRVARAIELEKLEKQSGEVPVHKLSLKKVQLQSEFCTAIRVQYMH 73
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ELTVVQPLTLDRVARAIELEKLEKQSGEVPVHKLSLKKVQLQSEFCTAIRVQYMH 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ITVNGCFEPRARATKATVAFAASEGHSHPRVVELPKTDGLGFGFNVGKGQNSPIY 133
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ITVNGCFEPRARATKATVAFAASEGHSHPRVVELPKTDGLGFGFNVGKGQNSPIY 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RIIPGVAERHGLKRGDQLLSVNGSVSVE 164
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RIIPGVAERHGLKRGDQLLSVNGVALE 151
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

PRELIMINARY; PRT; 195 AA.

(TREMBLrel. 13, Created)
(TREMBLrel. 13, Last sequence update)
(TREMBLrel. 24, Last annotation update)
sin.

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GN OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TAXID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer J
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chand
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., D
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischm
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchu
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.
RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese I
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Yao Q.A
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zhen
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smiti
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster. ";
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AE003750; AAF56389.1; -
DR HSSP; Q12959; 1PDR.
DR FlyBase; FBgn0039269; veli.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02828; L27; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00569; L27; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
SQ SEQUENCE 195 AA; 21493 MW; EF9DF5ED71A73FBC CRC64;

Query Match 64.4%; Score 754; DB 5; Length 195;
Best Local Similarity 77.9%; Pred.No.5.8e-53;
Matches 148; Conservative 20; Mismatches 22; Indels 0;

Qy 21 QPLTLDRVARAIELEKLEKQSGEVPVHKLSLKKVQLQSEFCTAIRVQYMH
Db 6 BELTSLDRVRSIELEKLEKQSGDFTTKLAALQKVLNSDFMTSVREYVHYE
Qy 81 CPEFRARATKATVAFAASEGHSHPRVVELPKTDGLGFGFNVGKGQNSPIY
Db 66 SHDVRASATKATVAFAASEGHSHPRVVELPKTEGLGFGFNVGKGQNSPIY

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CORINTHIOS 195

mansonii (Blood fluke).  
Nematoda; Platyhelminthes; Trematoda; Digenea; Strigeiida;  
oidea; Schistosomatidae; Schistosoma.  
183;

MM N.A.  
O Rican;  
14538; PubMed=10406037;  
Jouison P.S., Wilson R.A.;  
ation, cloning and immunogenicity of antigens released by  
larvae of Schistosoma mansoni.;  
/118-583-594(1999).  
ITY: CONTAINS 1 PDZ/DHR DOMAIN.  
465; AAB86566.1; -;  
5; 1BFE.  
342; P:intracellular signaling cascade; IEA.  
PR004172; L27.  
R001478; PDZ.  
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95; PDZ; 1.  
228; PDZ; 1.  
30106; PDZ; 1.  
protein.  
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71 AA; 19000 MW; 69685P4108598063 CRC64;

55.4%; Score 648.5; DB 5; Length 171;  
larity 73.7%; Pred.No. 1.5e-44;  
Conservative 26; Mismatches 17; Indels 1; Gaps 1;

VHKLQSLKVLQSEFCTAIREVYQYMHETITVNGCEFFARATATVAFAASEGH 103  
PSKLAALQILQSFCDMIREVYEHYITVDINGSEEVKASATATVAFAASEGH 63  
RVVLPKTDGLGPNVNGKQNSPIYISRIIPGVVAERHGLKGGQLLSVNGSV 163  
RVIELPKTNEGLGPNVNGKQNSPIYISRMXPGVADRHGLKGGQLLSVNGISV 123  
HHEKAVELLKAAKDSVKLVVRYTPKVLSEMEARPEKLTARRRQ 210  
HHERAVELLKAAQTVKLVVRYTPRILEMEARPEKLTARRRQ 169

PRELIMINARY; PRT; 316 AA.

(TrEMBLrel. 13, Created)  
(TrEMBLrel. 18, Last sequence update)  
(TrEMBLrel. 25, Last annotation update)  
protein.

is elegans.

Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
Peloderinae; Caenorhabditis.  
239;

MM N.A.

DEC-1998) to the EMBL/GenBank/DBJ databases.

MM N.A.  
19613; PubMed=9851916;

ence of the nematode C.elegans: A platform for  
ig biology.;  
2012-2018(1998).  
TY: CONTAINS 1 PDZ/DHR DOMAIN.  
188; CAA2459.2; -;  
127179.  
1; IPDR.

42; P:intracellular signaling cascade; IEA.

DR InterPro; IPR004172; L27.  
DR InterPro; IPR001478; PDZ.  
DR Pfam; PF02828; L27; 1.  
DR Pfam; PF00595; PDZ; 1.  
DR SMART; SM00569; L27; 1.  
DR SMART; SM00228; PDZ; 1.  
DR PROSITE; PS50106; PDZ; 1.  
SQ SEQUENCE 316 AA; 35663 MW; E050959F2D29BBFF CRC64;

Query Match 55.3%; Score 647.5; DB 5; Length 316;  
Best Local Similarity 67.9%; Pred.No. 4.1e-44;  
Matches 129; Conservative 30; Mismatches 30; Indels 1;

QY 25 LDRVARATELLEKQLQSEGVVPHKQLQSLKVLQSEFCTAIREVYQYMHETITV  
Db 117 LERDVQRILELMEHVQKTGEVNNAKLASLQVQLQSEFFGAVREVYETVYESIDA  
QY 85 RARATATVAFAASEGHSHPRVVELPKTDEGLGPNVNGKQNSPIYISRII  
Db 177 KAAATATVAFAAAGHAPRIVELPKTDGGLGPNVNGKQNSPIYISRII  
QY 145 RHGLKRGDQLSVNGSVGEHEKAVELLKAAKDSVKLVVRYTPKVLSEMEAR  
Db 237 RHGLKRGDQLSVNGSVGEHEKAVELLKAAKDSVKLVVRYTPKVLSEMEAR  
QY 205 TARRRQQQL 214  
Db 296 IRSTQQSPTL 305

RESULT 15

P90976 PRELIMINARY; PRT; 297 AA.  
AC P90976;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE LIN-7 (Fragment).  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabdito  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96200771; PubMed=8612272;  
RA Simeke J.S., Kaech S.M., Harp S.A., Kim S.K.;  
RT "LET-23 receptor localization by the cell junction protein LIN-7;  
RT during C. elegans vulval induction.";  
RL Cell 85:195-204(1996).  
CC 1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
DR EMBL; U78092; AAB36684.1; -;  
DR HSSP; Q12959; IPDR.  
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
DR InterPro; IPR004172; L27.  
DR InterPro; IPR001478; PDZ.  
DR Pfam; PF02828; L27; 1.  
DR Pfam; PF00595; PDZ; 1.  
DR SMART; SM00569; L27; 1.  
DR SMART; SM00228; PDZ; 1.  
DR PROSITE; PS50106; PDZ; 1.  
FT NON\_TER 297 297  
SQ SEQUENCE 297 AA; 33580 MW; A8F15EDB90B0A90E CRC64;

Query Match 55.0%; Score 643.5; DB 5; Length 297;  
Best Local Similarity 70.6%; Pred.No. 7.9e-44;  
Matches 127; Conservative 29; Mismatches 23; Indels 1;

QY 25 LDRVARATELLEKQLQSEGVVPHKQLQSLKVLQSEFCTAIREVYQYMHETITV  
Db 117 LERDVQRILELMEHVQKTGEVNNAKLASLQVQLQSEFFGAVREVYETVYESIDA  
QY 85 RARATATVAFAASEGHSHPRVVELPKTDEGLGPNVNGKQNSPIYISRII  
:

15:31:26 2004

us-09-909-005-1.rapt

AATAKATVAAFAAEGHAHPRIVELPKTDQGLGNMGGKQNSPIYISIIIPGGVAD 236

GGLKRGDOLLSVNGSVGEHEHKAVELLKAADSVKLVVRYTPKVLLEMEARFEKLR 204

GGLKRGDOLIAVNG-NVEAECHERKAVDLKSAVGSVKLVIRYMPKLLDENERRERQR 295

: March 18, 2004, 13:28:20  
CS

15:31:25 2004

us-09-909-005-1.rag

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

tein search, using sw model

March 18, 2004, 13:19:49 ; Search time 59 Seconds  
(without alignments)

1115.823 Million cell updates/sec

US-09-909-005-1

1170  
1 MLKPSVTSAPTADMATLVV.....ILLIQQQQQQQQQTQNHMS 233

BLOSUM62

Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues

hits satisfying chosen parameters: 1586107

length: 0  
length: 2000000000

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

A\_Geneseq\_23Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB	ID	Description
100.0	233	2	AA29978	Aay29978 Human cel
100.0	233	4	AAU07127	Aau07127 Human cel
100.0	233	5	AAU99326	Aau99326 Human cel
100.0	233	7	ADD46702	Add46702 Human Pro
100.0	233	7	AD55392	Ad55392 Human Pro
89.6	197	4	AAW78892	Aam78892 Human pro
89.6	197	4	AA93600	Aab93600 Human pro
89.6	198	4	AAW9876	Aam79876 Human pro
69.0	207	4	AAE03655	Aae03655 Human ext
69.0	207	5	AAU83629	Aau83629 Human PRO
69.0	207	6	ABU80776	Abu80776 Human PRO
69.0	207	6	ABO33742	Abo33742 Novel hum
69.0	207	6	ABU82085	Abu82085 Novel hum
69.0	207	6	ABJ72265	Abj72265 Novel hum
69.0	207	6	ABJ72393	Abj72393 Human PRO
69.0	207	6	ABO34288	Abo34288 Human sec
69.0	207	7	ABJ72095	Abj72095 Human mem
69.0	207	7	AB83566	Ab83566 Novel hum
69.0	207	7	ABU80672	Abu80672 Novel hum
69.0	207	7	ABD73213	Abd73213 Novel hum
69.0	207	7	ABD78295	Abd78295 Novel hum
69.0	207	7	ABD84943	Abd84943 Human PRO
69.0	207	7	ABD78049	Abd78049 Novel hum
69.0	207	7	ABD87115	Abd87115 Human PRO
69.0	207	7	ABD84697	Abd84697 Human PRO

26	807	69.0	207	7	ADB83812	Adb83812
27	807	69.0	207	7	ADB72967	Adb72967
28	807	69.0	207	7	ADC36805	Adc36805
29	807	69.0	207	7	ADC21795	Adc21795
30	807	69.0	207	7	ADC49826	Adc49826
31	807	69.0	207	7	ADC49025	Adc49025
32	807	69.0	207	7	ADC49542	Adc49542
33	807	69.0	207	7	ADC47403	Adc47403
34	807	69.0	207	7	ADC47148	Adc47148
35	807	69.0	207	7	ADC78023	Adc78023
36	807	69.0	207	7	ADD06258	Add06258
37	807	69.0	207	7	ADC77777	Adc77777
38	807	69.0	207	7	ADD50740	Add50740
39	807	69.0	207	7	ADD50986	Add50986
40	807	69.0	207	7	ADD50467	Add50467
41	807	69.0	207	7	ADD50221	Add50221
42	807	69.0	207	7	ADD51232	Add51232
43	807	69.0	207	8	ADC48779	Adc48779
44	807	69.0	207	8	ADE20950	Ade20950
45	807	69.0	207	8	ADE05794	Ade05794

#### ALIGNMENTS

RESULT 1  
AA29978  
ID AAY29978 standard; protein; 233 AA.  
XX  
AC AAY29978;  
XX  
DT 23-NOV-1999 (first entry)  
XX  
DE Human cell junction PDZ protein CUPDZ.  
XX  
KW Human; cell junction PDZ protein; PDZ domain; CUPDZ; diagnosis;  
KW neurological disorder; developmental disorder; William's syndr  
XX  
OS Homo sapiens.  
XX  
PN US5959731-A.  
XX  
PD 28-SEP-1999.  
XX  
PF 11-SEP-1998; 98US-00151611.  
XX  
PR 11-SEP-1998; 98US-00151611.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
PI Yue H, Patterson C, Au-Young J;  
XX  
DR WPI; 1999-561035/47.  
DR N-PSDB; AA221259.  
XX  
PT Nucleic acids encoding cellular junction PDZ protein domains us  
PT the prevention, diagnosis and treatment of disorders associated  
PT defective cell signaling such as cancers and neurological and  
PT developmental disorders.  
XX  
PS Claim 1; Col 39-40; 27pp; English.  
XX  
CC The present sequence represents human cell junction PDZ protein  
CC CUPDZ polynucleotides and proteins may be used in the diagnosis  
CC prevention and treatment of disorders associated with defective  
CC signalling. They may be used to treat cancers, neurological dis  
CC developmental disorders such as William's syndrome. CUPDZ or ve  
CC containing CUPDZ may be administered to treat any of the above  
CC by rectifying mutations or deletions in a patient's genome that  
CC cell signalling by expressing inactive proteins or to supplemen  
CC patients own production of CUPDZ protein domains. Antisense nuc  
CC molecules may be administered to down regulate CUPDZ protein dc  
CC expression by binding with the cells own CUPDZ genes and preven

1. **CONCLUSIONS**

11-SEP-1998. 09115-00151617

RESULT 3	
AAU99326	
ID	AAU99326 standard; protein; 233 AA.
XX	
AC	AAU99326;
XX	
DT	07-OCT-2002 (first entry)
XX	
DE	Human cell junction PDZ (CYPDZ) protein.
XX	
KW	Human; cytostatic; nontropic; neuroprotective; endocrine;
KW	cell junction PDZ; CYPDZ; membrane-associated signalling protein
KW	signal transduction; postsynaptic density protein 95; PSD-95; ZC
KW	Drosophila lethal (1) discs large-1; Dlg; zonula occludens-1; ZC
KW	cell signalling; cancer; leukaemia; lymphoma; neurological disorder
KW	Alzheimer's disease; Parkinson's disease; developmental disorder
KW	muscular dystrophy; William's syndrome.
XX	
OS	Homo sapiens.
XX	
OS	
XX	
Key	Location/Qualifiers
FT	107..189
Domain	/note= "Putative PDZ domain"
FT	
XX	
US	US2002082388-A1.
XX	
27-JUN-2002.	
PD	
XX	
PF	18-JUL-2001; 2001US-00909005.
XX	
PR	11-SEP-1998; 98US-00151611.
XX	

us-09-909-005-1.rag

; neuronal tissue; gene therapy;  
ental nerve injury; chronic constriction injury; CCI;  
e injury; SNI; Chung.

|||||  
LVVRYTPKVLMEARFEKLTARRRQQQLLIQQQQQQQQQQQQQQQNHMS 233

indard; protein; 233 AA.

(first entry)

in NP\_004655, SEQ ID NO 1207.

: neuronal tissue; gene therapy;  
: antal nerve injury; chronic constriction injury; CCI;  
: injury; SNI; Chung.

3.

3-A2.

: 2002WO-US025765.

: 2001US-0312147P.

: 2001US-0346382P.

: 2001US-0333347P.

HOSPITAL CORP.

XR AG.

urso D, Befort K, Costigan M;

: 8312/26.

: 004655.

: ion comprising two or more isolated polypeptides, useful for  
: medicament for treating pain in an animal.

re; 1017pp; English.

on discloses a composition comprising two or more isolated rat  
ynucleotides or a polynucleotide which represents a fragment,  
r allelic variation of the nucleic acid sequence. Also  
a vector comprising the novel polynucleotide, a host cell  
he vector, a method for identifying a nucleotide sequence  
ferentially regulated in an animal subjected to pain and a  
rm the method, an array, a method for identifying an agent  
es or decreases the expression of the polynucleotide sequence  
erentially expressed in neuronal tissue of a first animal  
ain, a method for identifying a compound which regulates  
on of a polynucleotide sequence which is differentially  
an animal subjected to pain, a method for identifying a  
t regulates the activity of one or more of the  
des, a method for producing a pharmaceutical composition, a  
identifying a compound or small molecule that regulates the  
an animal of one or more of the polypeptides given in the  
n, a method for identifying a compound useful in treating  
harmaceutical composition comprising the one or more  
or their antibodies. The polynucleotide or the compound that  
s activity is useful for preparing a medicament for treating  
pinal segmental nerve injury (Chung), chronic constriction  
and spared nerve injury (SNI) in an animal (e.g. gene  
e sequence presented is a human protein (shown in Table 2 of  
action) which is differentially expressed during pain. Note:  
: data for this patent did not form part of the printed  
n, but was obtained in electronic form directly from WIPO at  
/pub/published\_pt\_sequences.

AA;

Query Match 100.0%; Score 1170; DB 7; Length 233;  
Best Local Similarity 100.0%; Pred No. 7.5e-108;  
Matches 233; Conservative 0; Mismatches 0; Indels 0;  
  
QY 1 MKPSVTSAPTADMATLVQPLTLDRDVARAIELLEKLQESGEVPHVKLSLKI  
Db 1 MKPSVTSAPTADMATLVQPLTLDRDVARAIELLEKLQESGEVPHVKLSLKI  
  
QY 61 FCTAIREVYQYVHETITVNGCPFRARATAKATVAAFAAEGHSHPRVVEPKTI  
Db 61 FCTAIREVYQYVHETITVNGCPFRARATAKATVAAFAAEGHSHPRVVEPKTI  
  
QY 121 NVMGKEQNSPIYISRIIPGGVAERHGGKRGDQLLSVNGSVSVEGHEHEKAVEL  
Db 121 NVMGKEQNSPIYISRIIPGGVAERHGGKRGDQLLSVNGSVSVEGHEHEKAVEL  
  
QY 181 SVKLIVRYTPKVLMEARFEKLTARRRQQQLLIQQQQQQQQQQQQQQQNHMS ;  
Db 181 SVKLIVRYTPKVLMEARFEKLTARRRQQQLLIQQQQQQQQQQQQQQQNHMS ;

# RESULT 6

AAW78892

ID AAW78892 standard; protein; 197 AA.

XX AC AAW78892;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 1554.

XX XX

KW Human; cytokine; cell proliferation; cell differentiation; gene  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesi  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PR 20-JUN-2000; 2000US-00598075.

XX PR 19-JUL-2000; 2000US-00620325.

XX PR 01-SEP-2000; 2000US-00654936.

XX PR 15-SEP-2000; 2000US-00663561.

XX PR 20-OCT-2000; 2000US-00693325.

XX PR 30-NOV-2000; 2000US-00728422.

XX PA (HYSE-) HYSEQ INC.

XX XX

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, We

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

DR WPI; 2001-476283/51.

DR N-PSDB; AAK52025.

XX XX

PT Nucleic acids encoding polypeptides with cytokine-like activitie  
PT in diagnosis and gene therapy.

XX PS Claim 20; Page 3872-3873; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and  
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity e  
CC cytokine, cell proliferation or cell differentiation or which ma  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vac  
CC peptide therapy. The polypeptides have various cytokine-like act



all growth factor activity, haematopoiesis regulating  
issue growth factor activity, immunomodulatory activity and  
in activity and may be useful in the diagnosis and/or  
f cancer, leukaemia, nervous system disorders, arthritis and  
n. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
and 3666 (AAM80020) are omitted as the relevant pages from the  
sing were missing at the time of publication

7 AA;

69.6%; Score 814; DB 4; Length 197;

ilarity 80.6%; Pred. No. 1.6e-72;

Conservative 24; Mismatches 13; Indels 0; Gaps 0;

LTLDRVARAIELEKLOSGEVPVHKLQSLKVKVQSEFCTAIREVVOYVHTIIVNG 80  
VLELDRICRAIELEKLOSGEVPVHKLQSLKVKVQSEFCTAIREVVOYVHTIIVNG 80  
VLELDRICRAIELEKLOSGEVPVHKLQSLKVKVQSEFCTAIREVVOYVHTIIVNG 80

EFAPATAKATVAAPAAASEGSHPRVVELPKTDGEGFNVGKGQNSPIYISRIIPG 140  
SVANATAKATVAAPAAASEGSHPRVVELPKTDGEGFNVGKGQNSPIYISRIIPG 140  
SVANATAKATVAAPAAASEGSHPRVVELPKTDGEGFNVGKGQNSPIYISRIIPG 140

AERHGGKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEARF 200  
ADRHGGKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEARF 200  
ADRHGGKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEARF 200

XTARRQQ 211  
MESAKRQQ 196

andard; protein; 197 AA.

(first entry)

in sequence SEQ ID NO:13038.

ar; detection; diagnosis; antisense therapy; gene therapy.

3.

2.

2000EP-00116126.

99JP-00248036.

99JP-00300253.

2000JP-00118776.

2000JP-00183767.

2000JP-00241899.

EX RES INST.

rai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
giyama T, Wakamatsu A, Nagai K, Otsuki T;

18749/34.

for synthesizing polynucleotides, particularly the 5602 full-  
s defined in the specification, and for the detection and/or  
s the abnormality of the proteins encoded by the full-length

ID NO 13038; 2537pp + Sequence Listing; English.

vention describes primer sets for synthesising 5602 full-  
s defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to  
complementary strand of a polynucleotide which comprises one of  
nucleotide sequences defined in the specification, where the  
oligonucleotide comprises at least 15 nucleotides; or (b) a com  
of an oligonucleotide comprising a sequence complementary to th  
complementary strand of a polynucleotide which comprises a 5'-e  
sequence and an oligonucleotide comprising a sequence complemen  
polynucleotide which comprises a 3'-end sequence, where the  
oligonucleotide comprises at least 15 nucleotides and the combi  
the 5'-end sequence/3'-end sequence is selected from those defi  
specification. The primer sets can be used in antisense therapy  
gene therapy. The primers are useful for synthesising polynucle  
particularly full-length cDNAs. The primers are also useful for  
detection and/or diagnosis of the abnormality of the proteins e  
the full-length cDNAs. The primers allow obtaining of the full-  
cDNAs easily without any specialised methods. AAH03166 to AAH13  
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 t  
represent human amino acid sequences; and AAH13629 to AAH13632  
oligonucleotides, all of which are used in the exemplification  
present invention  
XX Sequence 197 AA;  
SQ

Query Match 69.6%; Score 814; DB 4; Length 197;

Best Local Similarity 80.6%; Pred. No. 1.6e-72;

Matches 154; Conservative 24; Mismatches 13; Indels 0;

QY 21 QPLTLDRVARAIELEKLOSGEVPVHKLQSLKVKVQSEFCTAIREVVOYVHTIIVNG 80  
DB 6 EPLRLERDICRAIELEKLOSGEVPVHKLQSLKVKVQSEFCTAIREVVOYVHTIIVNG 80  
QY 81 CPEFRARATATVAAPAAASEGSHPRVVELPKTDGEGFNVGKGQNSPIYI 211  
DB 66 SPEVRANATATVAAPAAASEGSHPRVVELPKTDGEGFNVGKGQNSPIYI 211  
QY 141 GVAERHGGKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEARF 200  
DB 126 GIADRHGGKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEARF 200  
QY 201 EXLRTARRQQ 211  
DB 186 EERSAKRQQ 196

RESULT 8

AAM79876

ID AAM79876 standard; protein; 198 AA.

XX AAM79876;

XX 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 3522.

XX Human; cytokine; cell proliferation; cell differentiation; gene  
vaccine; peptide therapy; stem cell growth factor; haematopoies  
tissue growth factor; immunomodulatory; cancer; leukaemia;  
nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX 20-JUN-2000; 2000US-00598075.

XX 19-JUL-2000; 2000US-00620325.

XX 01-SEP-2000; 2000US-00654936.

XX 15-SEP-2000; 2000US-00663561.

us-09-909-005-1.rag

[illegible]



enoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;  
2045/32.  
6878.

and twenty two nucleic acids encoding PRO polypeptides,  
he manufacture of a medicament for diagnosing or treating

g 76; 314pp; English.

invention relates to the isolation of novel human PRO  
, and the polynucleotide sequences encoding them. The PRO  
are secreted and transmembrane proteins. The PRO  
and polynucleotides are useful for preparing a medicament  
e diagnosis and treatment of tumours. Anti-PRO antibodies are  
agnostic assays for PRO, by detecting its expression in  
is, tissues or serum, and for affinity purification of PRO  
nant cell culture or natural sources. AB080739-AB080860  
e human PRO polypeptides of the invention. Note: The sequence  
s patent was obtained in electronic format directly from the  
te at [seqdata.uspto.gov/psipspIDentry.html](http://seqdata.uspto.gov/psipspIDentry.html)

AA;

69.0%; Score 807; DB 6; Length 207;  
larity 78.5%; Pred. No. 8.4e-72;  
Conservative 24; Mismatches 17; Indels 2; Gaps 1;

LTWVPLTDRDVARAIELEKQESGEVPHVKLSKLVQSEFCTATREVVQYMH 73  
L--VEPLGLEDVDSRAVELLERLQSGELPPQKLQALQVLRFCSAIREVQYLI 58  
TVNGCPERAPATAKATAVAAPAASEGHSHPRVVELPKTDEGLGFNVNGKQNSPIY 133  
DITGSAETRAHATAKATAVAFTAASEGHSHPRVVELPKTDEGLGFNVNGKQNSPIY 118  
IIPGGVAERHGLKRGDQLLSVNGSVSGEGHEKAVELLKAAKDSVKLVVTPKVL 193  
VIPGGVADRHGGLKRGDQLLSVNGSVSGEGHEKAVELLKAAQGSVKLVVTPKVL 178  
EARFEXKLRTARRRQQQQ 213  
EARFEXKMSARRRQQHQ 198

ndard; protein; 207 AA.

(first entry)

secreted and transmembrane protein PRO10200.

ted and transmembrane protein; PRO; cytostatic;  
c; osteopathic; gene therapy; TNF-Agonist-Alpha;  
stimulator; pericyte stimulator; fibroblast modulator;  
al; diagnostic; biosensor; bioreactor; tumour; lung tumour;  
; breast tumour; prostate tumour; rectal tumour;  
; bone disorder; cartilage disorder; sports injury;  
ound.

-Al.

2002US-00218631.

XX 01-JUN-2001; 2001WO-US017800.  
XX 29-JUN-2001; 2001WO-US021066.  
XX 09-APR-2002; 2002US-00119480.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, W  
XX WPI; 2003-512315/48.  
XX DR N-PSDB; ACD68630.  
XX New genes, and its encoded secreted and transmembrane polypeptid  
PT useful for stimulating tumor Necrosis Factor alpha, or chondrocy  
PT pericyte proliferation, especially for treating lung tumors, art  
PT wounds in a mammal.

Claim 11; Fig 76; 314pp; English.

The invention describes an isolated nucleic acid molecule compri  
sequence with at least 80% identity to: (a) a nucleotide encodin  
122 PRO (secreted and transmembrane) polypeptides whose sequence  
fully defined in the specification; or (b) any of 122 nucleotide  
sequences having e.g. 4834, 2504 or 1759 bp fully defined in the  
specification; or the full length coding sequence of any these 1  
nucleotide sequences. The PRO polypeptides or polynucleotides ar  
as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
particularly useful for detecting tumours (e.g. lung tumour, col  
tumour, breast tumour, prostate tumour, rectal tumour, or liver  
in a mammal, for stimulating the release of TNF-alpha from human  
for stimulating the proliferation or differentiation of chondroc  
cells for stimulating proliferation of pericyte cells, or for a  
normal human dermal fibroblast proliferation. The PRO nucleic ac  
polypeptide is also useful for treating tumours or various bone  
cartilage disorders (e.g. sports injuries or arthritis), or woun  
PRO polypeptides are useful in drug screening, particularly as t  
for therapeutic intervention in these diseases, and in the diagn  
determination of the presence of these diseases. The PRO polypef  
also useful as molecular weight markers, or for chromosome  
identification. The PRO genes are useful as hybridisation probes  
screening libraries of human cDNA, genomic DNA or mRNA. The PRO  
also be used in gene therapy, particularly for replacing a defec  
gene. This is the amino acid sequence of a novel human secreted  
transmembrane PRO polypeptide

SQ Sequence 207 AA;

Query Match 69.0%; Score 807; DB 6; Length 207;  
Best Local Similarity 78.5%; Pred. No. 8.4e-72;  
Matches 157; Conservative 24; Mismatches 17; Indels 2;

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Db 1 MAAL--VEPLGLEDVDSRAVELLERLQSGELPPQKLQALQVLRFCSAIREV 178  
QY 74 ETTIVNGCPERAPATAKATAVAAPAASEGHSHPRVVELPKTDEGLGFNVNGKQEQ 193  
Db 59 DTLDTGSAETRAHATAKATAVAFTAASEGHSHPRVVELPKTDEGLGFNVNGKQEQ 178  
QY 134 ISRIIPGGVAERHGLKRGDQLLSVNGSVSGEGHEKAVELLKAAKDSVKLVVRY 193  
Db 119 ISRVIPGGVADRHGGLKRGDQLLSVNGSVSGEGHEKAVELLKAAQGSVKLVVRY 178  
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ID ABU82085 standard; protein; 207 AA.  
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XX	ABJ72265;		
DT	06-NOV-2003 (first entry)		
XX	Human PRO10200 protein.		
XX	PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte		
KW	differentiation; dermal fibroblast; tumour; gene therapy; cytoe		
OS	Homo sapiens.		
XX	US2003050448-A1.		
XX	13-MAR-2003.		
XX	28-AUG-2002; 2002US-00230414.		
XX	01-JUN-2001; 2001WO-US017800.		
PR	29-JUN-2001; 2001WO-US021066.		
PR	09-APR-2002; 2002US-00119480.		
XX	(GETH ) GENENTECH INC.		
PA	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU,		
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, v		
PT	WPI; 2003-521818/49.		
DR	N-FSDB; ABT44263.		
XX	New nucleic acid encoding for a PRO protein, useful for the man		
PT	of a medicament for diagnosing or treating tumors or for measur		
PT	detecting expression of an associated gene.		
XX	Claim 11; Fig 76; 315pp; English.		
PS	The invention relates to a novel isolated nucleic acid encoding		
CC	defined PRO polypeptide. The molecules of the invention may be i		
CC	stimulating proliferation or gene expression in pericyte cells c		
CC	release of TNF-alpha from human blood. Other possible uses incl		
CC	stimulation or inhibition of chondrocyte proliferation or		
CC	differentiation, the stimulation of human dermal fibroblast cell		
CC	proliferation and the detection of the presence of a tumour wit		
CC	mammal. Furthermore, the nucleic acid may be useful for the man		
CC	of a medicament for diagnosing or treating a tumour within a ma		
CC	for measuring or detecting the expression of an associated gene,		
CC	as during gene therapy. The current sequence is that of the huma		
CC	protein of the invention		
XX	Sequence 207 AA;		
SQ	Query Match 69.0%; Score 807; DB 6; Length 207;		
	Best Local Similarity 78.5%; Pred.No.8.4e-72;		
	Matches 157; Conservative 24; Mismatches 17; Indels 2;		
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Db	59	DILDITSAIRAHATAKAIVTAFTASEGAHPRVPELPKTDEGLGFNIMGREK	
QY	134	IGRIIPGVAEHRGGIKRGDQLISVNGSVGEHHEKAVELLKAAKDSVKLVLRV	

Search completed: March 18, 2004, 13:26:52  
Job time : 61 secs

Standard; protein; 207 AA.

-A1.

VTECH INC.

in encoding nucleic acid, useful for preparing PRO and anti-PRO antibodies for detecting the presence of a animal.

relates to a novel isolated PRO protein encoding nucleic acid of the invention may be useful for preparing PRO and anti-PRO antibodies for detecting the presence of a tumour. Furthermore, the molecules of the invention may be used to stimulate proliferation or gene expression in pericyte release of tumour necrosis factor (TNF)-alpha from human pericyte cells, proliferation or differentiation of chondrocyte cells and for the proliferation of normal human dermal fibroblast cells. The molecules may be utilised during gene therapy. The current state of the art of the human PRO protein of the invention

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15:31:25 2004

us-09-909-005-1.rapb

GenCore version 5.1.6  
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IS-09-909-005-1

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length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

SUMMARIES

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69.0	207	12	US-10-219-535-76	Sequence 76, Appl	
69.0	207	12	US-10-232-230-76	Sequence 76, Appl	
69.0	207	14	US-10-227-884-76	Sequence 76, Appl	
69.0	207	14	US-10-230-163-76	Sequence 76, Appl	
69.0	207	14	US-10-149-819-19	Sequence 19, Appl	
69.0	207	14	US-10-230-338-76	Sequence 76, Appl	
69.0	207	14	US-10-218-631-76	Sequence 76, Appl	
69.0	207	14	US-10-230-414-76	Sequence 76, Appl	
69.0	207	14	US-10-216-159A-76	Sequence 76, Appl	
69.0	207	14	US-10-218-849-76	Sequence 76, Appl	
69.0	207	14	US-10-227-873-76	Sequence 76, Appl	
69.0	207	14	US-10-227-883-76	Sequence 76, Appl	
69.0	207	14	US-10-219-076-76	Sequence 76, Appl	
69.0	207	14	US-10-230-434-76	Sequence 76, Appl	

16	807	69.0	207	14	US-10-219-003-76	Sequence
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ALIGNMENTS

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; Patent No. US20020082388A1  
; GENERAL INFORMATION:  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Patterson, Chandra  
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN  
; FILE REFERENCE: PF-0599 US  
; CURRENT APPLICATION NUMBER: US/09/309,005  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/370,1  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-06  
; SOFTWARE: PERL Program  
; NUMBER OF SEQ ID NOS: 3  
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; FEATURE: -  
; OTHER INFORMATION: 1974337  
US-09-909-005-1

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noyers, Luc  
ritsen, Mary  
ddard, Audrey  
owski, Paul J.  
imaldi, J. Christopher  
mey, Austin L.  
ich, Victoria  
ephan, Jean-Philippe F.  
tanabe, Colin L.  
od, William I.  
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PRIOR FILING DATE: 1999-01-12

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us-09-909-005-1.rapb

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ATE: 1999-01-12  
ION NUMBER: 60/115733  
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69.08; Score 807; DB 14; Length 207;

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; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU  
; FILE REFERENCE: P3530P1C96  
; CURRENT APPLICATION NUMBER: US/10/230,163  
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; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
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; PRIOR FILING DATE: 1998-06-25

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Query Match 69.0%; Score 807; DB 14; Length 207;  
Best Local Similarity 78.5%; Pred. No. 5.5e-70;  
Matches 157; Conservative 24; Mismatches 17; Indels 2;  
QY 14 MATLTVQPLTDRDVARAIELLEKLOESGEVPHKLOSLKKVLOSEFCTAIRE  
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLOALQORVLQSFCSAIRE  
QY 74 EITVNGCPFERARATKATVAFAASEGSHPRVVELPKTDEGLGNVMGCKE

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DITSAETRAHATAKATVAATFASGHAHPRVVELPKTDEGLGNMGKEQNSPIY 118
IIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRYTPKVL 193
VIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRYTPKVL 178
EAPFEKLTARRRQQOQ 213
EAPFEKLTARRRQQOQ 198

plication US/10149819
US20030044913A1
TION:
YTE GENOMICS, INC.
E, Henry
IMZAI, Yalda
NG, Y. Tom
TTERSON, Chandra
UGHN, Mariah R.
, Dyung Aina M.
AH, Purvi
L, Preeti
-YOUNG, Janice
RFORD, Neil
TION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
: PF-0760 PCT
ATION NUMBER: US/10/149,819
DATE: 2002-06-10
ION NUMBER: 60/172,852; 60/172,354
ATE: 1999-12-10; 1999-12-16
ID NOS: 42
: Program

o sapiens
c.feature
TION: Incyte ID No. US20030044913A1 4062841CD1

69.0%; Score 807; DB 14; Length 207;
larity 78.5%; Pred. No. 5.5e-70;
Conservative 24; Mismatches 17; Indels 2; Gaps 1;

LTVVQPLTLDNRVARAIELEKLGESGVPVHKLQSLKVLQSEFCTAIRV 73
L--VEPLGLERDVSRAVELLERLQSGELPPQKQALQRLVLSRFSAIRV 58
TVNGCFEERARATATVAFAASEGHSHPRVVELPKTDEGLGNMGKEQNSPIY 133
DITGSAETRAHATAKATVAATFASGHAHPRVVELPKTDEGLGNMGKEQNSPIY 118
IIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRYTPKVL 193
VIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRYTPKVL 178
EAPFEKLTARRRQQOQ 213
EAPFEKLTARRRQQOQ 198

plication US/10230338
US20030044934A1
TION:
er, Kevin P.
enoyers, Luc
eritsen, Mary

Query Match 69.0%; Score 807; DB 14; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.5e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2;

Qy 14 MATLTVVQPLTLDNRVARAIELEKLGESGVPVHKLQSLKVLQSEFCTAIRV
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKQALQRLVLSRFSAIRV
Qy 74 ETITVNGCFEERARATATVAFAASEGHSHPRVVELPKTDEGLGNMGKEQ
Db 59 DTLDTITGSAETRAHATAKATVAATFASGHAHPRVVELPKTDEGLGNMGKEQ
Qy 134 ISRIIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRY
Db 119 ISRVIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRY
Qy 194 EEMEARFEKLTARRRQQOQ 213
Db 179 EEMEARFEKLTARRRQQOQ 198

RESULT 8
US-10-218-631-76
; Sequence 76, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
```

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PAL
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-76

Query Match 69.0%; Score 807; DB 14; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.5e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2;

Qy 14 MATLTVVQPLTLDNRVARAIELEKLGESGVPVHKLQSLKVLQSEFCTAIRV
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKQALQRLVLSRFSAIRV
Qy 74 ETITVNGCFEERARATATVAFAASEGHSHPRVVELPKTDEGLGNMGKEQ
Db 59 DTLDTITGSAETRAHATAKATVAATFASGHAHPRVVELPKTDEGLGNMGKEQ
Qy 134 ISRIIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRY
Db 119 ISRVIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVRY
Qy 194 EEMEARFEKLTARRRQQOQ 213
Db 179 EEMEARFEKLTARRRQQOQ 198

RESULT 8
US-10-218-631-76
; Sequence 76, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
```

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us-09-909-005-1.rapb

ney, Austin L.  
th, Victoria  
ephan, Jean-Philippe F.  
tanabe, Colin L.  
od, William I.  
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TION: ACIDS ENCODING THE SAME  
: P3530PIC14  
ATION NUMBER: US/10/218,631  
: DATE: 2002-08-12  
ION NUMBER: 10/119,480  
ATE: 2002-04-09  
ION NUMBER: 60/059113  
ATE: 1997-09-17  
ION NUMBER: 60/062287  
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ION NUMBER: 60/063549  
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ION NUMBER: 60/064103  
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ION NUMBER: 60/069873  
ATE: 1997-12-17  
ION NUMBER: 60/078910  
ATE: 1998-03-20  
ION NUMBER: 60/079294  
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ION NUMBER: 60/079656  
ATE: 1998-03-26  
ION NUMBER: 60/079728  
ATE: 1998-03-27  
or Application data removed - See File Wrapper or PALM.  
ID NOS: 246

io Sapien

69.0%; Score 807; DB 14; Length 207;  
larity 78.5%; Pred. No. 5.5e-70;  
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LTVVQPLTDRVARALELLEKLOESGVPVHKLOSLKVKLOSEFCTAIREVYQVMH 73  
L--VEPLGLERDVSRAVELLERLQSGELPKQKQALQRLVLSRFSALREVEQY 58  
TVNGCPEFRATATKATVAAPAAASEGHSHPRVVELPKTDEGLGFNVGKGQNSPIY 133  
DITGSAEIRAHATAKATVAAPAAASEGHSHPRVVELPKTDEGLGFNVGKGQNSPIY 118  
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VTPGVVADRHGGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVKLVYTPKVL 178  
EAFEFKLTARRRQQQ 213  
EAFEFKMSARRRQQH 198

pplication US/10230414  
US2003005048A1  
TION:  
cer, Kevin P.  
snoyers, Luc  
ritsen, Mary  
ddard, Audrey  
dowski, Paul J.  
imaldi, J. Christopher  
rney, Austin L.  
ith, Victoria  
-ephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NI  
FILE REFERENCE: P3530PIC98  
CURRENT APPLICATION NUMBER: US/10/230,414  
CURRENT FILING DATE: 2002-08-28  
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PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
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PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
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NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 76  
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ORGANISM: Homo Sapien  
US-10-230-414-76

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Qy 74 ETIVNGCPEFRATATKATVAAPAAASEGHSHPRVVELPKTDEGLGFNVGKGKE  
Db 59 DITGSAEIRAHATAKATVAAPAAASEGHSHPRVVELPKTDEGLGFNVGKGKE  
Qy 134 ISRIIPGVVAERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVKLVYR  
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RESULT 10  
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Sequence 76, Application US/10216159A  
Publication No. US20030069397A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NI

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; ION NUMBER: 60/059113
; ATE: 1997-09-17
; ION NUMBER: 60/062287
; ATE: 1997-10-17
; ION NUMBER: 60/063549
; ATE: 1997-10-28
; ION NUMBER: 60/064103
; ATE: 1997-10-31
; ION NUMBER: 60/069873
; ATE: 1997-12-17
; ION NUMBER: 60/078910
; ATE: 1998-03-20
; ION NUMBER: 60/079294
; ATE: 1998-03-25
; ION NUMBER: 60/079656
; ATE: 1998-03-26
; ION NUMBER: 60/079728
; ATE: 1998-03-27
; Application data removed - See File Wrapper or PALM.
; ID NOS: 246

; Sapien

69.0%; Score 807; DB 14; Length 207;
arity 78.5%; Pred. No. 5.5e-70;
onservative 24; Mismatches 17; Indels 2; Gaps 1;

; TVVQPLTDRVARAIELEKLOESGEVPHVKLSKVLQSEFCTAIREVYMH 73
; --VEPLGLERDVSRVAVELLERLQSGELPPQKLOALQVRVLSQSFCSAIREVYQLY 58
; NVNCPFRARATATAVAFAASEGHSHPRVVELPKTDEGLGNVWGKQNSPIY 133
; ITGSABIRAHATATAKATVAFTAASEGHAHPRVVELPKTDEGLGNVWGKQNSPIY 118
; IIPGVARHGGLKRGDQLSVNGSVSGEHEKAVELLKAAKDSVKLVVRYTPKVL 193
; IIPGVADRHGGLKRGDQLSVNGSVSGEHEKAVELLKAAQGSVKLVVRYTPRVL 178
; ARFEKLTARRRQOOQ 213
; ARFEKWSARRRQHQ 198

; Application US/10218849
; US20030073814A1
; ION:
; ar, Kevin P.
; snoyers, Luc
; critsen, Mary
; idard, Audrey
; lowski, Paul J.
; imaldi, J. Christopher
; ney, Austin L.
; ith, Victoria
; sphan, Jean-Philippe F.
; -anabe, Colin L.
; -ad, William I.
; ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ION: ACIDS ENCODING THE SAME
; : P3530P1C11
; ATION NUMBER: US/10/218,849
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; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-218-849-76

Query Match 69.0%; Score 807; DB 14; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.5e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2;

QY 14 MATLVQPLTDRVARAIELEKLOESGEVPHVKLSKVLQSEFCTAIREV
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QY 74 ETITVNGCPFRARATATAKATVAFTAASEGHSHPRVVELPKTDEGLGNVWGKQEQ
Db 59 DTLDTGSAEIRAHATATAKATVAFTAASEGHAHPRVVELPKTDEGLGNVWGKQEQ
QY 134 ISRIIPGVARHGGLKRGDQLSVNGSVSGEHEKAVELLKAAKDSVKLVVRY
Db 119 ISRVIPGVADRHGGLKRGDQLSVNGSVSGEHEKAVELLKAAQGSVKLVVRY
QY 194 EMEARPEKLTARRRQOOQ 213
Db 179 EMEARPEKWSARRRQHQ 198

RESULT 12
US-10-227-873-76
; Sequence 76, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
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ON NUMBER: 60/084441  
ATE: 1998-05-06  
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ON NUMBER: 60/085579  
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ON NUMBER: 60/086392  
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ON NUMBER: 60/089532  
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ATE: 1998-06-24  
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TION:  
er, Kevin P.  
snovers, Luc  
ritsen, Mary  
ddard, Audrey  
dowski, Paul J.  
imaldi, J. Christopher  
rney, Austin L.  
ith, Victoria  
ephan, Jean-Philippe F.  
tanabe, Colin L.  
od, William I.  
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TION: ACIDS ENCODING THE SAME  
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND N
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/151.611
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; GENERAL INFORMATION:  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Yong, Janice

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APPLICANT: Patterson, Chandra  
TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN

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; FILE REFERENCE: PF-0599 US  
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; CURRENT APPLICATION NUMBER: US/09/370,102

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; LENGTH: 297

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OTHER INFORMATION: q1685067

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Best Local Similarity 70.68: Pred. No. 2e-56:

STAVIT / CZ  
CZYTOWNOŚĆ / CZ  
KATEGORIA / CZ

[illegible]

THE  
FEDERAL  
BUREAU  
OF  
INVESTIGATION  
OF  
THE  
DEPARTMENT  
OF  
JUSTICE  
WASHINGTON, D. C. 20535

[illegible]

IT TYPICALLY TOOK AN AVERAGE OF 10 TO 15 MINUTES TO RECOVER FROM THE EFFECTS OF THE DRUGS.

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## RESULT 5

; Sequence 21, Application US/09562737

**GENERAL INFORMATION:**

APPLICANT: Gotthardt, Michael

; FILE REFERENCE: UTSW0708

; CURRENT FILING DATE: 2000-05-01

; SOFTWARE: PatentIn Ver. 2.1

; LENGTH: 724

; ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-562-737-21

Query Match 16.8%; Score 196.5; DB 4; Length 724;

Matches 41; Conservative 19; Mismatches 38; Indels 1;

106 PRVVELPKTDEGLGFNMGKEQNSPIYISRIIPGGVAERHGGGLKRGDQLLSVNG  
QY

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3E: Floppy disk  
IBM PC compatible

APPLICATION NUMBER: US/09/100.

us-09-909-005-1.rai

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QY 106 PAVVELPKTDEGLGVNMGCKEQNSPIYTSRIIPGVVAEBEGCLKRGDQLLSVNV
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Db 311 PRRIVHRGTTGLGFNV-GVEDEGIFISWLAGGPADYGLKRGQJIASVWG
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 166 EHHEKAVELLKAAKQSVKLAVRYTPKVLMEEARPEKLR 204
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 370 DSHEQAALENAGQVTIIIFQYKPEYSRGEAKIHLR 408
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent NO. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzn, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gonez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERA
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-12

Query Match 15.4%; Score 180.5; DB 3; Length 2466;
Best Local Similarity 27.9%; Pred. No. 1e-08; Indels 37;
Matches 51; Conservative 31; Mismatches 64;

QY 22 PUTLDRDVARAIELLEKLQESGVPVHKLQSLKKVLOSEFCTAIRVYQYMHETI
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Db 993 PQTVAELVKGPFHOMSRSDAESLAGVTKLNNKSV-----f-----EGIGFA
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QY 82 PPRPARATAKATV-----AAPASGSHGHPRVVELPKTD-----EGIGFA
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Db 1034 PRRKHSDSSDSSDGGQAYVLVDVHKRWSIVSSPEREITLVNKKDQYGLGFC
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QY 127 EQ---NSPTIYSRIIPGVVAERHGLKRGDQLLSVNGSVSGEHEHEKAVELLKAF
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Db 1094 KMGRLDGLGFISSVARGPPADFHGCLKPGDRLLSVNSVLSLGVSHHAAEILQNL
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QY 184 LVV 186
    : :
Db 1154 LVI 1156

RESULT 11
US-09-566-076-12
; Sequence 12, Application US/09566076
; Patent NO. 6475775
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzn, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gonez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERA
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/566,076
; CURRENT FILING DATE:
; EARLIER APPLICATION NUMBER: 09/080,855
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 39

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us-09-909-005-1.rai

R SEQ ID NO: 16:  
 RACTERISTICS:  
 7 amino acids  
 no acid  
 SS: single  
 linear  
 E: peptide  
 : NO  
 NO

Search completed: March 18, 2004, 13:29:27  
Job time : 23 secs